

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 16:44:13 ; Search time 4314.97 Seconds
(without alignments)
11614.233 Million cell updates/sec

Title: US-09-826-581-3

Perfect score: 1722

Sequence: 1 cctggccctcagatcaaga.....gatgagagctcggtcgga 1722

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 15

Total number of hits satisfying chosen parameters: 69629

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl.*

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9: gb_pr.*
10: gb_ro.*
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12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vi.*
30: em_htg_hum.*
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33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rod.*
36: em_htg_mam.*
37: em_htg_vrt.*
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39: em_htgo_hum.*
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41: em_htgo_other.*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1722	100.0	1722	6	AX281580	Sequence
C 2	1670	97.0	152129	2	AC027416	AC027416 Homo sapi
C 3	1479	85.9	206854	9	AC009974	AC009974 Homo sapi
4	168	9.8	1647	6	AX281582	Sequence
5	168	9.8	2109	6	AX099776	AX099776 Sequence
6	168	9.8	2115	6	AX099802	Sequence
7	168	9.8	2115	9	AF214519	AF214519 Homo sapi
8	168	9.8	2290	9	HS242937	HS242937 Homo sapi
9	57	3.3	106	11	G67375	G67375 A898 Human
C 10	39	2.3	227724	2	AF336381	AF336381 Mus muscu
11	38	2.2	1867	6	AX099774	AX099774 Sequence
12	38	2.2	1873	4	AF214520	AF214520 Sus scrof
13	38	2.2	1873	6	AX099800	Sequence
14	38	2.2	1873	6	AX398331	Sequence
15	38	2.2	1873	6	AX398333	Sequence
16	38	2.2	1873	6	AX398335	Sequence
17	38	2.2	1873	6	AX398337	Sequence
18	38	2.2	1873	6	AX398339	Sequence
19	38	2.2	2022	6	AX099804	Sequence
20	38	2.2	5888	4	AF214521	AF214521 Sus scrof
C 21	35	2.0	146577	2	AC128070	Rattus no
C 22	35	2.0	190183	2	AC129703	Rattus no
C 23	35	2.0	192968	2	AC127107	Rattus no
C 24	29	1.7	192968	2	AC127107	Rattus no
C 25	25	1.5	186248	2	AC026021	Homo sapi
C 26	25	1.5	216497	9	HSDJ37C10	AL049569 Human DNA
27	24	1.4	1328	10	RNMFKGAM	X95578 R. norvegicu
28	24	1.4	1550	10	RNU42413	U42413 Rattus norv
C 29	24	1.4	5946	10	RATNESTIN	M34384 Rat nestin
C 30	24	1.4	184288	2	AC129422	AC129422 Rattus no
C 31	23	1.3	1194	9	AB046627	AB046627 Macaca fa
C 32	23	1.3	81704	9	AL512353	AL512353 Human DNA
C 33	23	1.3	82806	9	AC007111	AC007111 Homo sapi
34	23	1.3	192180	2	AC023331	AC023331 Homo sapi
C 35	23	1.3	196413	2	AC009269	AC009269 Pan trogl
C 36	23	1.3	198172	2	AC009065	AC009065 Homo sapi
37	23	1.3	239434	2	AC012171	AC012171 Homo sapi
38	22	1.3	74645	2	AC128292	AC128292 Rattus no
C 39	22	1.3	138312	9	AC026353	AC026353 Homo sapi
C 40	22	1.3	238325	2	AC105847	AC105847 Rattus no
C 41	21	1.2	2079	10	BC019836	BC019836 Mus muscu
42	21	1.2	41680	10	AF049091	AF049091 Mus muscu
43	21	1.2	58725	9	AC003988	AC003988 Human PAC
44	21	1.2	63680	2	AC101117	AC101117 Mus muscu
C 45	21	1.2	78215	2	AC105803	AC105803 Rattus no

ALIGNMENTS

RESULT 1
AX281580
LOCUS AX281580 1722 bp DNA linear PAT 03-NOV-2001
DEFINITION Sequence 3 from Patent WO0177305.
ACCESSION AX281580
VERSION AX281580.1 GI:16608831
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL

Andersson, L., Luthman, H. and Marklund, S.
Variants of the human amp-activated protein kinase gamma 3 subunit
Patent: WO 0177305-A 3 18-OCT-2001;

FEATURES		Arexis AB (SE)		Location/Qualifiers	
source		1..1722		/organism="Homo sapiens"	
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Best Local Similarity 100.0%; Pred. No. 0;					
Matches 1722; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
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DB	1	CTTGGCCCTCAGATCAAGAAGCCCTTTTGTCTCTGTGGCCCAACGGGTGTGGGCGACG	60		
QY	61	CCCTCTATGGCAGCAGCAAGNAGCAGAGCTTTTGTGGGTGAGGAGGCTGGGAGGTGAAG	120		
DB	61	CCCTCTATGGCAGCAGCAAGNAGCAGAGCTTTTGTGGGTGAGGAGGCTGGGAGGTGAAG	120		
QY	121	GGAGATGGAGGAGGTGAGGGGAGATCTTTGTACGGTTGTCTGGGCTGATCTCTGATAT	180		
DB	121	GGAGATGGAGGAGGTGAGGGGAGATCTTTGTACGGTTGTCTGGGCTGATCTCTGATAT	180		
QY	181	ACCACAGCTTGGCTTTCAGGCCAAGCCAGCCAGGGCCAGGGGCTGAGGAAAGTCCATCC	240		
DB	181	ACCACAGCTTGGCTTTCAGGCCAAGCCAGCCAGGGCCAGGGGCTGAGGAAAGTCCATCC	240		
QY	241	GGAGTCTGATGGCAGCTGGGAGACCCCTGGGGCTCAATTTCCCATCTGTGGAGCCGCT	300		
DB	241	GGAGTCTGATGGCAGCTGGGAGACCCCTGGGGCTCAATTTCCCATCTGTGGAGCCGCT	300		
QY	301	ATGACAGCTGACACTTTTACCTCCGCTACTGCTATGCGCTTGTGCGCTGATAGTGCTAGG	360		
DB	301	ATGACAGCTGACACTTTTACCTCCGCTACTGCTATGCGCTTGTGCGCTGATAGTGCTAGG	360		
QY	361	AGCAATGGGGAGGAGGAG	420		
DB	361	AGCAATGGGGAGGAGGAG	420		
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DB	421	ACTGTCTCTTCCACAGTCCCCCTCTGCTCTGCTACGCTGCTGCTGCTGCTGCTGCTGCT	480		
QY	481	GGGATCTGACCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCT	540		
DB	481	GGGATCTGACCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCT	540		
QY	541	CTCCCTCTGACGGATGCTGACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	600		
DB	541	CTCCCTCTGACGGATGCTGACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	600		
QY	601	GGTCCCCCTGGTAGGAGTGGGCTGGGAATCTTATGGGCAACCCAGAGGGCGGGGGCGG	660		
DB	601	GGTCCCCCTGGTAGGAGTGGGCTGGGAATCTTATGGGCAACCCAGAGGGCGGGGGCGG	660		
QY	661	AGGGAGTCTCTCTGGAGCTGGTCCCTAGAACCCACAGTCTTCTGACTTCTGGAGTC	720		
DB	661	AGGGAGTCTCTCTGGAGCTGGTCCCTAGAACCCACAGTCTTCTGACTTCTGGAGTC	720		
QY	721	CTGTGATGCTCTAGGTCCAGATCTATGAGATTGAACAACATAGGATTCGAGCTGGAG	780		
DB	721	CTGTGATGCTCTAGGTCCAGATCTATGAGATTGAACAACATAGGATTCGAGCTGGAG	780		
QY	781	GGGTAGTGGGAGAGAAACCCGAAAGGGCTTGTGGTATGGTGGGCGAGGCTTTAAG	840		
DB	781	GGGTAGTGGGAGAGAAACCCGAAAGGGCTTGTGGTATGGTGGGCGAGGCTTTAAG	840		
QY	841	GTGGAGATGGGAGTGGGATGCTCTGGAGTGAACAGGGGAGGAGCAATAGAGCCCTCG	900		
DB	841	GTGGAGATGGGAGTGGGATGCTCTGGAGTGAACAGGGGAGGAGCAATAGAGCCCTCG	900		
QY	901	GGTGCCTGACGGAGGGAAGCTGCTGGGACTGCAAGGTGAGGAGGTGACCGGCTCCCC	960		
DB	901	GGTGCCTGACGGAGGGAAGCTGCTGGGACTGCAAGGTGAGGAGGTGACCGGCTCCCC	960		
QY	961	TGGCCTGACTCTGGCTCTTTTCTGAGAGATCTACTGCAAGGCTGCTGCTGCTGCTGCTGCT	1020		
DB	961	TGGCCTGACTCTGGCTCTTTTCTGAGAGATCTACTGCAAGGCTGCTGCTGCTGCTGCTGCT	1020		
QY	1021	CTCCATCTCTCTTAATGATAGGTGGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1080		
DB	1021	CTCCATCTCTCTTAATGATAGGTGGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1080		
QY	1081	ACAGTCTCCCTTCCAGTCCCACTCAGCTCTGAACTCACTTCTTCACTTCTTCACTTCTTCACT	1140		
DB	1081	ACAGTCTCCCTTCCAGTCCCACTCAGCTCTGAACTCACTTCTTCACTTCTTCACTTCTTCACT	1140		
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DB	1681	CGAATGTGTACCCACCCAGGATGAGAGGCTGCGGCTGGA	1722		
RESULT 2					
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LOCUS					
DEFINITION					
Homo sapiens clone RP11-504G11, WORKING DRAFT SEQUENCE, 32					
unorderd pieces.					
AC027416					
AC027416.2 GI:8317289					
HTG: HTGS_PHASE1; HTGS_DRAFT.					
SOURCE					
Homo sapiens					
ORGANISM					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE					
1 (bases 1 to 152129)					
AUTHORS					
Birren, B., Linton, L., Nusbaum, C. and Lander, E.					
TITLE					
Homo sapiens, clone RP11-504G11					
JOURNAL					
Unpublished					
REFERENCE					
2 (bases 1 to 152129)					

AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavsky, L., Boukhgater, B., Brown, A., Burkett, G., Campoliano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collimore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Hearford, A., Horton, L., Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Larocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lieu, G., Liu, G., Locke, K., MacDonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meidrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T. M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

TITLE

JOURNAL

COMMENT

Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 7, 2000 this sequence version replaced gi:7342115.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence.submissions@genome.wi.mit.edu

----- Project Information

Center project name: L7458

Center clone name: 504_G.11

----- Summary Statistics

Sequencing vector: M13; M7815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 135376 bases at least Q40

Consensus quality: 143264 bases at least Q30

Consensus quality: 146503 bases at least Q20

Insert size: 161000; agarose-fp

Quality coverage: 3.1 in Q20 bases; agarose-fp

Quality coverage: 3.3 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 1005: contig of 1005 bp in length
1006 1105: gap of 100 bp
1106 2402: contig of 1297 bp in length
2403 2502: gap of 100 bp
2503 3823: contig of 1321 bp in length
3824 3923: gap of 100 bp
3924 5020: contig of 1097 bp in length
5021 5120: gap of 100 bp
5121 6161: contig of 1041 bp in length
6162 6261: gap of 100 bp
6262 7547: contig of 1286 bp in length
7548 7647: gap of 100 bp
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9984 10083: gap of 100 bp
10084 12556: contig of 2473 bp in length
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15144 17123: contig of 1980 bp in length
17124 17223: gap of 100 bp
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22029 24319: contig of 2291 bp in length
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46466 51285: contig of 4820 bp in length
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77116 77215: gap of 100 bp
77216 85022: contig of 7807 bp in length
85023 85122: gap of 100 bp
85123 93314: contig of 8192 bp in length
93315 93414: gap of 100 bp
93415 101193: contig of 7779 bp in length
101194 101293: gap of 100 bp
101294 113090: contig of 11797 bp in length
113091 113190: gap of 100 bp
113191 123496: contig of 10306 bp in length
123497 123596: gap of 100 bp
123597 137837: contig of 14241 bp in length
137838 137937: gap of 100 bp
137938 152129: contig of 14192 bp in length.

FEATURES

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Query Match 97.0%; Score 1670; DB 2; Length 152129;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CCTGGCCCTCAGATCAAGAGGCTTCTTTGTCTGTGGTGGCCAAAGGTGTGGGGCAGC 60
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Qy 121 GGAGATCGAGGAGGTGAGGGGAGATCTTGACGGTTGTTCTGGGCTGATCTCTGATAT 180
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Qy 181 ACCACAAGCTTGCTTCAGGCCAAGCCAGCCAGGGGCCAGGGTGGAGAAAGTCCATCC 240
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Qy 301 ATGACGAGTGAACCTTTACCTCCGCTACTGCAATGGCCCTGTGCCATAGGTGCTAGGG 360
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Db 36258 AGCAATGGGGGAGCGAGAGAAAGACCCCACTTCTCAGGCTTGGGGGCTGCCCC 36199
Qy 421 ACTGTCTCTGTTCCACAGTCCCCACTGTGTCTCAGCACAAAGACACTGGCAGGGTGGGA 480

Db 36198 ACTGTCTCTGTTCCACAGTCCCACACTGTGTCTCASCACAAGGACACTGGCAGGGTGGGA 36139
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Db 36138 GGGGATCTGACCTCAACCTGCTTCCACCCAAAGGCCCGGGGTGACTCTCTCCCGCC 36079
Qy 541 CCTCCCTGCAAGGATGCTGACCATCACTGACTTCACTCTGGTGTGCTGATCGCTACTACA 600
Db 36078 CCTCCCTGCAAGGATGCTGACCATCACTGACTTCACTCTGGTGTGCTGATCGCTACTACA 36019
Qy 601 GGTCCCCCTGTGAGGAGTGGGTGGGAATCTTATGGGCACCCAGAGGGCGGGGGCGG 660
Db 36018 GGTCCCCCTGTGAGGAGTGGGTGGGAATCTTATGGGCACCCAGAGGGCGGGGGCGG 35959
Qy 661 AGGGAGTCTCTCTGAGCCTGGTGCCTAGAGCCACAGCTTCTTCTGACTTCTGGAGTC 720
Db 35958 AGGGAGTCTCTCTGAGCCTGGTGCCTAGAGCCACAGCTTCTTCTGACTTCTGGAGTC 35899
Qy 721 CTGTGATGTCTTAGGTCCAGATCTATGAGATTGAACAACATAGATTGAGACCTGGAG 780
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Qy 841 GTGAGGATGGGAGTGGGATGTCTTGAGTGAACAGGGAGGGAACAATAGGAGCTCG 900
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Qy 1441 CCTAGAGTCTGGGGAAGAGCTGGAGCCCTCTTGAAGCTGTGGATCCCTGATCTCC 1500
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QY 1681 CGAATGTGTACCCACCCAGGATGAGAGGCTCGGGCTGG 1721
Db 34938 CGAATGTGTACCCACCCAGGATGAGAGGCTCGGGCTGG 34898

RESULT 3
AC009974/c
LOCUS AC009974 206854 bp DNA linear PRI 09-JAN-2002
DEFINITION Homo sapiens BAC clone RP11-459119 from 2, complete sequence.
ACCESSION AC009974
VERSION AC009974.9 GI:16799058
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Sulston,J.E. and Waterston,R.
1 (bases 1 to 206854)
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 206854)
AUTHORS Harris,A. and Certon,M.
TITLE The sequence of Homo sapiens BAC clone RP11-459119
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 206854)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 4 (bases 1 to 206854)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (08-NOV-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 5 (bases 1 to 206854)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 6 (bases 1 to 206854)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Nov 8, 2001 this sequence version replaced gi:13431203.
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Center: Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@wustl.wustl.edu
-----
Summary Statistics
Center project name: H_NH0459119
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPC1-11 human BAC library was made from the blood of one male donor, as described by Otagawa,K., Moon,P.Y., Zhao,B., Frengen,E., Tateo,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this clone is at base position 1 of RP11-459119; actual end is at base position 206854 of RP11-459119.

Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 and AC009974. A single plasmid region exists between 38812-38903. An unresolved tandem in the HEAV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing.

FEATURES

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Db 165559 CAGACAAGGAGCCTTGGTGGCCCTCCCTCTCTTTTGGGGCTCGGATGGAGGTGTCT 165500

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QY 1441 CCCTAGCAGTCTGTGGGAGAGCTGGGAGCCTCTTGAAGCTGTGGATCCCTGATCTCC 1500

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QY 1561 TATCCAGATTTGGCATCGGCACATTCAGACATTCGCTGTGTGCTGGAGCAGCAC 1620

Db 165139 TATCCAGATTTGGGCATCGGCACATTCAGACATTCGCTGTGTGCTGGAGCAGCAC 165080

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QY 1681 CGAATGTGTATCCACCCAGGATGAGAGCTCGGCTGG 1721

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RESULT 4

AX281582

LOCUS AX281582 1647 bp DNA linear PAT 02-NOV-2001

DEFINITION Sequence 5 from Patent WO0177305.

ACCESSION AX281582

VERSION AX281582.1 GI:16608833

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1

TITLE Variants of the human amp-activated protein kinase gamma 3 subunit

JOURNAL Patent: WO 0177305-A 5 18-OCT-2001; Arexis AB (SE)

FEATURES

source Location/Qualifiers

1. .1647

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20. .1489

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BASE COUNT 346 a 502 c 462 g 337 t

ORIGIN

Query Match 9.8%; Score 168; DB 6; Length 1647;

Best Local Similarity 100.0%; Pred. No. 2.6e-78;

Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1523 GGTTCCTGCTGCCCGCCCTCTCTCTACCGCACTATCCAAGATTTGGGCATCGGC 1582

Db 1022 GGTTCCTGCTGCCCGCCCTCTCTCTACCGCACTATCCAAGATTTGGGCATCGGC 1081

QY 1583 ACATTCGAGACTTGGCTGTGGTGGAGACAGACACCCATCTCTGACTGGACATC 1642

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QY 1643 TTTGTGAGCGGCTGTCTGCACTGCCCTGTGTCGTCACCAAGATGTGGT 1690

Db 1142 TTTGTGAGCGGCTGTCTGCACTGCCCTGTGTCGTCACCAAGATGTGGT 1189

RESULT 5

AX099776

LOCUS AX099776 2109 bp DNA linear PAT 02-APR-2001

DEFINITION Sequence 3 from Patent WO0120003.

ACCESSION AX099776

VERSION AX099776.1 GI:13538810

KEYWORDS human.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 2109)

Rogel-Gaillard, C., Looft, C., Kalm, E., Milan, D., Robic, A.,

Chardon, P.

Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof

Patent: WO 0120003-A 3 22-MAR-2001;

INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ; Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)

FEATURES

Location/Qualifiers

1. .2109

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ORIGIN

Query Match 9.8%; Score 168; DB 6; Length 2109;

Best Local Similarity 100.0%; Pred. No. 2.5e-78;

Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
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 DEFINITION
 AX099802
 ACCESSION
 AX099802.1 GI:13538836
 VERSION
 KEYWORDS
 SOURCE

ORGANISM
 Homo sapiens
 human.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 2115)
 Anderson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,
 Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
 Chardon, P.
 Variants of the gamma chain of ampk, dna sequences encoding the
 same, and uses thereof
 Patent: WO 0120003-A 29 22-MAR-2001;
 INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
 Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
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BASE COUNT
 ORIGIN
 Query Match 9.8%; Score 168; DB 6; Length 2115;
 Best Local Similarity 100.0%; Pred. No. 2.5e-78;
 Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1523 GGTTCCTGCTGCCCCCGCCCTCTCTTACCGCAGATCCCAAGATTTGGGCATCGGC 1582
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QY 1583 ACATTCCGAGACTTGCTGTGCTGGAGAGCAGACCCATCTGACTGCATCGACATC 1642
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 Db 988 ACATTCCGAGACTTGCTGTGCTGGAGAGCAGACCCATCTGACTGCATCGACATC 1047
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QY 1643 TTTGTGGACCGCGTGTGCTGCACCTGCTGTGGTCAACGAATGTGGT 1690
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 Db 1048 TTTGTGGACCGCGTGTGCTGCACCTGCTGTGGTCAACGAATGTGGT 1095
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 AF214519
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 DEFINITION
 Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3)
 mRNA, complete cds.

QY 1523 GGTTCCTGCTGCCCCCGCCCTCTCTTACCGCAGATCCCAAGATTTGGGCATCGGC 1582
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 HSA249977
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 mRNA, complete cds.

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 Db 928 GGTTCCTGCTGCCCCCGCCCTCTCTTACCGCAGATCCCAAGATTTGGGCATCGGC 987
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 LOCUS
 HSA249977
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 mRNA, complete cds.

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 Db 1048 TTTGTGGACCGCGTGTGCTGCACCTGCTGTGGTCAACGAATGTGGT 1095
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 HSA249977
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 mRNA, complete cds.

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 Db 928 GGTTCCTGCTGCCCCCGCCCTCTCTTACCGCAGATCCCAAGATTTGGGCATCGGC 987
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 HSA249977
 DEFINITION
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 mRNA, complete cds.

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 mRNA, complete cds.

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 Db 928 GGTTCCTGCTGCCCCCGCCCTCTCTTACCGCAGATCCCAAGATTTGGGCATCGGC 987
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QY 1643 TTTGTGGACCGCGTGTGCTGCACCTGCTGTGGTCAACGAATGTGGT 1690
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ACCESSION
 VERSION
 KEYWORDS
 SOURCE

ORGANISM
 Homo sapiens
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 2115)
 Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A., Thelander, M.,
 Rogel-Gaillard, C., Paul, S., Iannuccelli, N., Raak, L., Ronne, H.,
 Lundstrom, K., Reinsch, N., Gellin, J., Kalm, E., Roy, P.L., Chardon, P.
 and Andersson, L.
 A mutation in PRKAG3 associated with excess glycogen content in pig
 skeletal muscle
 Science 288 (5469), 1248-1251 (2000)
 20280150
 PUBMED
 10818001

REFERENCE
 AUTHORS

TITLE

JOURNAL
 MEDLINE
 20280150
 PUBMED
 10818001

REFERENCE
 AUTHORS

TITLE

JOURNAL
 Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
 University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
 Sweden

FEATURES
 source

1. .2115
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 460 a 622 c 562 g 471 t

BASE COUNT
 ORIGIN

Query Match 9.8%; Score 168; DB 9; Length 2115;
 Best Local Similarity 100.0%; Pred. No. 2.5e-78;
 Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 928 GGTTCCTGCTGCCCCCGCCCTCTCTTACCGCAGATCCCAAGATTTGGGCATCGGC 987
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QY 1583 ACATTCCGAGACTTGCTGTGCTGGAGAGCAGACCCATCTGACTGCATCGACATC 1642
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 Db 988 ACATTCCGAGACTTGCTGTGCTGGAGAGCAGACCCATCTGACTGCATCGACATC 1047
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QY 1643 TTTGTGGACCGCGTGTGCTGCACCTGCTGTGGTCAACGAATGTGGT 1690
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 Db 1048 TTTGTGGACCGCGTGTGCTGCACCTGCTGTGGTCAACGAATGTGGT 1095
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RESULT 8
 HSA249977
 LOCUS
 HSA249977
 DEFINITION
 Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3)
 mRNA, complete cds.

QY 1523 GGTTCCTGCTGCCCCCGCCCTCTCTTACCGCAGATCCCAAGATTTGGGCATCGGC 1582
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 Db 928 GGTTCCTGCTGCCCCCGCCCTCTCTTACCGCAGATCCCAAGATTTGGGCATCGGC 987
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QY 1583 ACATTCCGAGACTTGCTGTGCTGGAGAGCAGACCCATCTGACTGCATCGACATC 1642
 |||||
 Db 988 ACATTCCGAGACTTGCTGTGCTGGAGAGCAGACCCATCTGACTGCATCGACATC 1047
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QY 1643 TTTGTGGACCGCGTGTGCTGCACCTGCTGTGGTCAACGAATGTGGT 1690
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 Db 1048 TTTGTGGACCGCGTGTGCTGCACCTGCTGTGGTCAACGAATGTGGT 1095
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RESULT 9
 HSA249977
 LOCUS
 HSA249977
 DEFINITION
 Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3)
 mRNA, complete cds.

QY 1523 GGTTCCTGCTGCCCCCGCCCTCTCTTACCGCAGATCCCAAGATTTGGGCATCGGC 1582
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QY 1583 ACATTCCGAGACTTGCTGTGCTGGAGAGCAGACCCATCTGACTGCATCGACATC 1642
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 Db 1048 TTTGTGGACCGCGTGTGCTGCACCTGCTGTGGTCAACGAATGTGGT 1095
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RESULT 10
 HSA249977
 LOCUS
 HSA249977
 DEFINITION
 Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3)
 mRNA, complete cds.

QY 1523 GGTTCCTGCTGCCCCCGCCCTCTCTTACCGCAGATCCCAAGATTTGGGCATCGGC 1582
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 Db 928 GGTTCCTGCTGCCCCCGCCCTCTCTTACCGCAGATCCCAAGATTTGGGCATCGGC 987
 |||||

QY 1583 ACATTCCGAGACTTGCTGTGCTGGAGAGCAGACCCATCTGACTGCATCGACATC 1642
 |||||
 Db 988 ACATTCCGAGACTTGCTGTGCTGGAGAGCAGACCCATCTGACTGCATCGACATC 1047
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QY 1643 TTTGTGGACCGCGTGTGCTGCACCTGCTGTGGTCAACGAATGTGGT 1690
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 Db 1048 TTTGTGGACCGCGTGTGCTGCACCTGCTGTGGTCAACGAATGTGGT 1095
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RESULT 11
 HSA249977
 LOCUS
 HSA249977
 DEFINITION
 Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3)
 mRNA, complete cds.

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 |||||
 Db 928 GGTTCCTGCTGCCCCCGCCCTCTCTTACCGCAGATCCCAAGATTTGGGCATCGGC 987
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QY 1583 ACATTCCGAGACTTGCTGTGCTGGAGAGCAGACCCATCTGACTGCATCGACATC 1642
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 Db 988 ACATTCCGAGACTTGCTGTGCTGGAGAGCAGACCCATCTGACTGCATCGACATC 1047
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QY 1643 TTTGTGGACCGCGTGTGCTGCACCTGCTGTGGTCAACGAATGTGGT 1690
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 Db 1048 TTTGTGGACCGCGTGTGCTGCACCTGCTGTGGTCAACGAATGTGGT 1095
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RESULT 12
 HSA249977
 LOCUS
 HSA249977
 DEFINITION
 Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3)
 mRNA, complete cds.

QY 1523 GGTTCCTGCTGCCCCCGCCCTCTCTTACCGCAGATCCCAAGATTTGGGCATCGGC 1582
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 Db 928 GGTTCCTGCTGCCCCCGCCCTCTCTTACCGCAGATCCCAAGATTTGGGCATCGGC 987
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QY 1583 ACATTCCGAGACTTGCTGTGCTGGAGAGCAGACCCATCTGACTGCATCGACATC 1642
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QY 1643 TTTGTGGACCGCGTGTGCTGCACCTGCTGTGGTCAACGAATGTGGT 1690
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DEFINITION Homo sapiens mRNA for AMP-activated protein kinase gamma 3 subunit (AMPK gamma 3 gene).

ACCESSION AJ249977

VERSION AJ249977.1 GI:6688200

KEYWORDS AMP-activated protein kinase; AMPK gamma 3 gene; gamma 3 subunit.

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2290) Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Cheung,P.C., Salt,I.P., Davies,S.P., Hardie,D.G. and Carling,D.

TITLE Characterization of AMP-activated protein kinase gamma-subunit isoforms and their role in AMP binding

JOURNAL Biochem. J. 346 Pt 3, 659-669 (2000)

MEDLINE 20164049

PUBMED 10988692

REFERENCE 2 (bases 1 to 2290) Carling,D.

AUTHORS Direct Submission

TITLE Submitted (12-OCT-1999) Carling D., Cellular Stress Group, MRC Clinical Sciences Centre, Hammersmith Hospital, DuCane Road, London, W12 0NN, UNITED KINGDOM

JOURNAL Eukaryota

FEATURES

source Location/Qualifiers

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/organism="Homo sapiens"

/db_xref="taxon:9606"

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/gene="AMPK gamma 3"

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/function="AMP-activated protein kinase regulatory subunit"

/codon_start=1

/evidence=experimental

/product="AMP-activated protein kinase gamma 3 subunit"

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BASE COUNT 501 a 674 c 617 g 498 t

ORIGIN

Query Match 9.8%; Score 168; DB 9; Length 2290;

Best Local Similarity 100.0%; Pred. No. 2.4e-78;

Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1523 GGTTCCTGTCGCCCGCCCTCTCTCTACCGCACTATCCAGATTTGGGCATCGGC 1592

Db 1024 GGTTCCTGTCGCCCGCCCTCTCTCTACCGCACTATCCAGATTTGGGCATCGGC 1083

Qy 1593 ACATTCGAGACTTGGCTGCTGTGAGAGACAGACCCATCTCGACTGCACTGACATC 1642

Db 1084 ACATTCGAGACTTGGCTGCTGTGAGAGACAGACCCATCTCGACTGCACTGACATC 1143

Qy 1643 TTTGTGACCCGCGTGTGCTGTGCACTGCTGTGTCACGAATGTGGT 1690

Db 1144 TTTGTGACCCGCGTGTGCTGTGCACTGCTGTGTCACGAATGTGGT 1191

RESULT 9

G67375

LOCUS

DEFINITION A898 Human Homo sapiens STS genomic, sequence tagged site.

ACCESSION G67375

VERSION G67375.1 GI:11841655

KEYWORDS STS.

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 106) Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Robic,A., Jeon,J.-T., Rey,V., Amarger,V., Chardon,P., Looft,C., Anderson,L., Gellin,J. and Milan,D.

TITLE Construction of a high-resolution RH map of human 2q35 region on TNG panel and comparison with physical map of porcine homologous region 15q25

JOURNAL Unpublished (2001)

COMMENT Contact: Annie ROBIC, Denis MILAN

Genetique Cellulaire

Institut National de Recherche agronomique (INRA)

BP27, 31326 Castanet Tolosan, France

Tel: (33) 5 61 28 51 21

Fax: (33) 5 61 28 53 08

Email: arobic@coulouze.inra.fr

Primer A: TGGCATCGGCACATTC

Primer B: GACCACAGCAGTCAGCA

PCR Profile:

Initial incubation: 94 degrees C for 4 min

Denaturation: 94 degrees C for 30 seconds

Annealing: 55 degrees C for 30 seconds

Polymerization: 72 degrees C for 30 seconds

PCR cycles: 33

Thermal cycler: Perkin Elmer 9600

Protocol:

Template: 25 ng

Primer: each 0.5 uM

dNTPs: each 200 uM

Taq Polymerase: 0.1 units/reaction

Total Vol: 15 ul

Buffer:

MgCl2: 2 mM

KCl: 50 mM

Tris-HCl: 20 mM

pH: 8.4

Primers were defined on sequence AAL78898 (cDNA). No intron.

FEATURES

source Location/Qualifiers

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/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="Human"

STS

1..106

primer_bind 16 a 28 c 33 g 27 t 2 others

BASE COUNT 16 a 28 c 33 g 27 t 2 others

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2e-18;

Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 50 ATCTGACTGCACTGACATCTTTGTGGACCGCGTGTGTCTGCACTGCTGTGGTC 106

RESULT 10

AF336381/c

LOCUS

DEFINITION Mus musculus chromosome 1 clone PAC510; PAC457, *** SEQUENCING IN PROGRESS ***; 3 unordered pieces.

ACCESSION AF336381

VERSION AF336381.1 GI:13507298

KEYWORDS HTG; HTGS_PHASE1.

SOURCE Mus musculus.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Qy 1562 ATCCAAGATTGGGCATCGGCACATTCGAGACTTGGC 1599
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Db 967 ATCCAAGATTGGGCATCGGCACATTCGAGACTTGGC 1004
|||||

Search completed: January 7, 2003, 20:11:10
Job time : 4937.97 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 17:17:03 ; Search time 479,092 Seconds
(without alignments)
1486.844 Million cell updates/sec

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Perfect score: 1647
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Scoring table: OLIGO NUC
Gapop_60.0 , Gapext 60.0

Searched: 381593 seqs, 216252194 residues

Word size : 15

Total number of hits satisfying chosen parameters: 1247

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	168	10.2	1722	10	US-09-826-581-3
5	85	5.2	378	10	US-09-864-761-1373
6	54	3.3	92	10	US-09-864-761-20146
7	52	3.2	821	10	US-09-826-581-1
8	20	1.2	333	10	US-09-974-300-1402
9	19	1.2	1411	9	US-09-935-720-2
10	19	1.2	7771	9	US-09-832-292-38
11	18	1.1	153	10	US-09-864-761-22801
12	18	1.1	325	10	US-09-960-352-2438
13	18	1.1	394	10	US-09-867-701-968
14	18	1.1	459	10	US-09-864-761-6044
15	18	1.1	487	10	US-09-962-436-230
16	18	1.1	3364	10	US-09-880-107-1075
17	18	1.1	3364	10	US-09-925-300-665
18	18	1.1	6746	10	US-09-919-497-18
19	18	1.1	6746	10	US-09-967-768A-303

20	18	1.1	17849	10	US-09-764-847-1315	Sequence 1315, Ap
21	18	1.1	17862	10	US-09-764-847-1313	Sequence 1313, Ap
22	18	1.1	106323	10	US-09-803-661-3	Sequence 3, Appli
23	17	1.0	234	9	US-09-938-842A-642	Sequence 642, Appl
24	17	1.0	238	10	US-09-969-708-265	Sequence 26, Appl
25	17	1.0	240	10	US-09-834-975-685	Sequence 685, Appl
26	17	1.0	257	10	US-09-834-975-360	Sequence 360, App
27	17	1.0	303	9	US-09-738-626-1431	Sequence 1431, Ap
28	17	1.0	337	10	US-09-954-456-1746	Sequence 1746, Ap
29	17	1.0	341	9	US-10-046-935-561	Sequence 561, App
30	17	1.0	341	9	US-09-878-178-561	Sequence 561, App
31	17	1.0	342	9	US-09-738-626-1429	Sequence 1429, Ap
32	17	1.0	342	10	US-09-867-701-3768	Sequence 3768, Ap
33	17	1.0	360	10	US-09-954-456-546	Sequence 546, App
34	17	1.0	373	10	US-09-920-300A-794	Sequence 794, App
35	17	1.0	373	10	US-09-920-300A-1146	Sequence 1146, Ap
36	17	1.0	373	12	US-10-033-528-794	Sequence 794, App
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38	17	1.0	429	10	US-09-960-352-4139	Sequence 4139, App
39	17	1.0	445	10	US-09-998-598-904	Sequence 904, App
40	17	1.0	446	10	US-09-822-849A-153	Sequence 153, App
41	17	1.0	528	10	US-09-864-761-23804	Sequence 23804, A
42	17	1.0	576	10	US-09-764-877-860	Sequence 860, App
43	17	1.0	585	10	US-09-864-761-7073	Sequence 7073, Ap
44	17	1.0	777	10	US-09-974-300-6862	Sequence 6862, Ap
45	17	1.0	795	10	US-09-764-847-1727	Sequence 1727, Ap

ALIGNMENTS

RESULT 1

US-09-826-581-5

; Sequence 5, Application US/09826581

; Patent No. US20020142310A1

; GENERAL INFORMATION:

; APPLICANT: Andersson, Leif

; APPLICANT: Luchman, L. Holger

; APPLICANT: Marklund, Stefan

; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBU

; FILE REFERENCE: 11145-007001

; CURRENT APPLICATION NUMBER: US/09/826.581

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: US 60/195,665

; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 1647

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (20)...(1486)

US-09-826-581-5

Query Match 100.0%; Score 1647; DB 10; Length 1647;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTGCTCTGGGGCTGGCCACATGGAGCCCGGCTGGAGCAGCACTGGCGCAGGACCCCTTC 60

Qy 61 CTGAGCAGCCTTGGGGGTTCTGAGCATCAAGAGATGAGCTTCTTAGAGCAAGAAAACAG 120

Db 61 CTGAGCAGCCTTGGGGGTTCTGAGCATCAAGAGATGAGCTTCTTAGAGCAAGAAAACAG 120

Qy 121 CAGCTCATGGCCATCACCAGCTGTGACCAGCCTGAGAAAGAAATCGTGGGAAACGGAG 180

Db 121 CAGCTCATGGCCATCACCAGCTGTGACCAGCCTGAGAAAGAAATCGTGGGAAACGGAG 180

Qy 181 GGCCAAAGCCTTGAGATGGAGCAAGGAGAGTGGTGGAGGAGGGGAGCCACCGGTCA 240

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US-09-826-581-4
; Sequence 4, Application US/09826581
; Patent No. US2002014210A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Leif
; APPLICANT: Luthman, L. Holger
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT
; FILE REFERENCE: 11145-007001
; CURRENT APPLICATION NUMBER: US/09/826,581
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-581-4

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RESULT 4

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US-09-826-581-3
; Sequence 3, Application US/09826581
; Patent No. US20020142310A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Leif
; APPLICANT: Luthman, L. Holger
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT
; FILE REFERENCE: 11145-007001
; CURRENT APPLICATION NUMBER: US/09/826,581
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3

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RESULT 5

US-09-864-761-3373/C
; Sequence 3373, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
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; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117

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/ SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
/ SEQ ID NO 3373
/ LENGTH: 378
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: MAP TO AC009974.3
/ OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4
/ OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.1
/ OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4
/ OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.9
/ OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.8
/ OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.8
/ OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.3
/ OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.8
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.2
/ OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4
/ OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.1
/ OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4
/ OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.8
/ OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.8
/ OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.3
/ OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.8
/ OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.4
/ OTHER INFORMATION: NT HIT: G111430152, EVALUE 2.00e-22
/ OTHER INFORMATION: EST HUMAN HIT: BE327467.1, EVALUE 3.00e-06
/ OTHER INFORMATION: SWISSPROT HIT: P54619, EVALUE 3.00e-03
US-09-864-761-3373

Query Match      5.2%; Score 85; DB 10; Length 378;
Best Local Similarity 100.0%; Pred. No. 2.7e-32;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 651 AGATCAAGAAGGCTTCTTCTGCTGCGCCAAACGGTGTGGGGCAGCCCTCTATGGG 710
|||||
DB 351 AGATCAAGAAGGCTTCTTCTGCTGCGCCAAACGGTGTGGGGCAGCCCTCTATGGG 292
|||||

QY 711 ACAGCAAGAAGCAGAGCTTTGTGGG 735
|||||
DB 291 ACAGCAAGAAGCAGAGCTTTGTGGG 267
|||||

RESULT 6
US-09-864-761-20146/c
/ Sequence 20146, Application US/09864761
/ Patent No. US20020048763A1
/ GENERAL INFORMATION:
/ APPLICANT: Penn, Sharon G.
/ APPLICANT: Rank, David R.
/ APPLICANT: Hanzel, David K.
/ APPLICANT: Chen, Wensheng
/ TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
/ TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
/ FILE REFERENCE: Aemica-X-1
/ CURRENT APPLICATION NUMBER: US/09/864,761
/ CURRENT FILING DATE: 2001-05-23
/ PRIOR APPLICATION NUMBER: US 60/180,312
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: US 09/632,366
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661

Query Match      3.3%; Score 54; DB 10; Length 92;
Best Local Similarity 100.0%; Pred. No. 5.9e-17;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 651 AGATCAAGAAGGCTTCTTCTGCTGCGCCAAACGGTGTGGGGCAGCCCTC 704
|||||
DB 54 AGATCAAGAAGGCTTCTTCTGCTGCGCCAAACGGTGTGGGGCAGCCCTC 1
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RESULT 7
US-09-826-581-1
/ Sequence 1, Application US/09826581
/ Patent No. US20020142310A1
/ GENERAL INFORMATION:
/ APPLICANT: Andersson, Leif
/ APPLICANT: Luthman, L. Holger
/ APPLICANT: Marklund, Stefan
/ TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUB
/ FILE REFERENCE: 11145-007001
/ CURRENT APPLICATION NUMBER: US/09/826,581
/ CURRENT FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: US 60/195,665
/ PRIOR FILING DATE: 2000-04-07
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 821
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-826-581-1

Query Match      3.2%; Score 52; DB 10; Length 821;
Best Local Similarity 100.0%; Pred. No. 5.8e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGTCTGGGGCTGGCCACATGGAGCCCGGCTGGAGCAGCAGCTGCGCAGG 52
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DB 313 TTGGTCTGGGGCTGGCCACATGGAGCCCGGCTGGAGCAGCAGCTGCGCAGG 364
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RESULT 8
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US-09-974-300-1402
; Sequence 1402, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085 500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8491
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1402
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-1402

Query Match          1.2%, Score 20; DB 10; Length 333;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 GACCAGCGCTCAGAAAGAA 164
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Db 265 GACCAGCGCTCAGAAAGAA 284

RESULT 9
US-09-935-720-2
; Sequence 2, Application US/09935720
; Patent No. US20020156260A1
; GENERAL INFORMATION:
; APPLICANT: HIRANO, TOSHIO
; KAISHO, NISHINOMIYA
; TITLE OF INVENTION: GENE ENCODING A POLYPEPTIDE HAVING A
; PRE-B CELL GROWTH-SUPPORTING ABILITY
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCELLELAND, MAIER& NEUSTADT,
; P. C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/935,720
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/517,739
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/08/997,252
; FILING DATE: 23-DEC-1997
; APPLICATION NUMBER: US 08/537,942
; FILING DATE: 21-NOV-1995
; APPLICATION NUMBER: PCT/JP94/00819
; FILING DATE: 20-MAY-1994
; APPLICATION NUMBER: JP 5-141178
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
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; REFERENCE/DOCKET NUMBER: 4767-0005-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1411 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1..84
; IDENTIFICATION METHOD: /note= "IDENTIFICATION METHOD: E"
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-935-720-2

Query Match          1.2%, Score 19; DB 9; Length 1411;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1112 ACAGCACCCATCCTGACTG 1130
      |||||
Db 948 ACAGCACCCATCCTGACTG 966

RESULT 10
US-09-832-292-38/c
; Sequence 38, Application US/09832292
; Patent No. US20020177205A1
; GENERAL INFORMATION:
; APPLICANT: Ryazanov, Alexey
; TITLE OF INVENTION: MAMMALIAN ALPHA-KINASE PROTEINS, NUCLEIC ACIDS AND
; FILE REFERENCE: 601-1-098CIP
; CURRENT APPLICATION NUMBER: US/09/832,292
; CURRENT FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 09/632,131
; PRIOR FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 7771
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-832-292-38

Query Match          1.2%, Score 19; DB 9; Length 7771;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 203 AGGCAGAAAGTCGGTGAGG 221
      |||||
Db 4855 AGGCAGAAAGTCGGTGAGG 4837

RESULT 11
US-09-864-761-22801
; Sequence 22801, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
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;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: US 09/632,366
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 22801
;; LENGTH: 153
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC003104.1
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
;; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
;; OTHER INFORMATION: EST_HUMAN HIT: AW749933.1, EVALUATE 2.00e-71
;; OTHER INFORMATION: NT HIT: g11426182, EVALUATE 1.00e-71
US-09-864-761-22801

Query Match 1.1%; Score 18; DB 10; Length 153;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 737 ATGCTGACCATCACTGAC 754
Db 96 ATGCTGACCATCACTGAC 113
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RESULT 12
US-09-960-352-2438
;; Sequence 2438, Application US/09960352
;; Patent No. US20020137139A1
;; GENERAL INFORMATION:
;; APPLICANT: Warren, Wesley C.
;; APPLICANT: Teo, Nengbing
;; APPLICANT: Wyatt, John C.
;; APPLICANT: Mathialagan, Nagappan
;; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
;; MUSCLE AND FAT DEPOSITION

;; FILE REFERENCE: 16511.006/37-21(10298)C
;; CURRENT APPLICATION NUMBER: US/09/960,352
;; CURRENT FILING DATE: 2001-09-24
;; NUMBER OF SEQ ID NOS: 15112
;; SEQ ID NO 2438
;; LENGTH: 325
;; TYPE: DNA
;; ORGANISM: Bos taurus
;; FEATURE:
;; NAME/KEY: unsure
;; LOCATION: (240)
;; OTHER INFORMATION: unsure at all n locations
;; OTHER INFORMATION: Clone ID: 11-LIB3058-018-Q1-K1-C3
US-09-960-352-2438

Query Match 1.1%; Score 18; DB 10; Length 325;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 214 GGTGGAGGAGGGGAGCC 231
Db 18 GGTGGAGGAGGGGAGCC 35
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RESULT 13
US-09-867-701-968/c
;; Sequence 968, Application US/09867701
;; Patent No. US20020132237A1
;; GENERAL INFORMATION:
;; APPLICANT: Aglate, Paul A.
;; APPLICANT: Jones, Robert
;; APPLICANT: Harlocker, Susan L.
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;; FILE REFERENCE: 210121.497
;; CURRENT APPLICATION NUMBER: US/09/867,701
;; CURRENT FILING DATE: 2001-05-29
;; NUMBER OF SEQ ID NOS: 10912
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 968
;; LENGTH: 394
;; TYPE: DNA
;; ORGANISM: Homo sapien
;; FEATURE:
;; NAME/KEY: misc.feature
;; LOCATION: (1)...(394)
;; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-968

Query Match 1.1%; Score 18; DB 10; Length 394;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1627 GACACCAGCCTCTTAGTC 1644
Db 38 GACACCAGCCTCTTAGTC 21
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RESULT 14
US-09-864-761-6044
;; Sequence 6044, Application US/09864761
;; Patent No. US20020048763A1
;; GENERAL INFORMATION:
;; APPLICANT: Penn, Sharon G.
;; APPLICANT: Rank, David R.
;; APPLICANT: Hanzel, David K.
;; APPLICANT: Chen, Wensheng
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
;; FILE REFERENCE: Aomics-X-1
;; CURRENT APPLICATION NUMBER: US/09/864,761
;; CURRENT FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/180,312

; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 6044
; LENGTH: 459
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC003104.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
US-09-864-761-6044

Query Match 1.1%; Score 18; DB 10; Length 459;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 737 ATGCTGACCATCACTGAC 754
| | | | | | | | | | | | | | | | | | | | | |
Db 125 ATGCTGACCATCACTGAC 142

RESULT 15
US-09-962-436-230
; Sequence 230, Application US/09962436
; Patent No. US20020081301A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; TITLE OF INVENTION: Secs
; FILE REFERENCE: 689290-75
; CURRENT APPLICATION NUMBER: US/09/962,436
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,082

; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/234,924
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 230
; LENGTH: 487
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-436-230

Query Match 1.1%; Score 18; DB 10; Length 487;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 440 GCCACAGAGGCTGGGAG 457
| | | | | | | | | | | | | | | | | | | | | |
Db 53 GCCACAGAGGCTGGGAG 70

Search completed: January 7, 2003, 20:17:43
Job time : 492.092 secs

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OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 20:16:02 ; Search time 62.0864 Seconds
(without alignments)
8135.386 Million cell updates/sec

Title: US-09-826-581-5
Perfect score: 1647
Sequence: 1 tctgtctgggctggccaca.....acaccagctcttagtcttc 1647

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 15

Total number of hits satisfying chosen parameters: 737

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	19	1.2	1411	1	US-08-537-942A-2
2	19	1.2	1411	4	US-08-997-252A-2
3	19	1.2	1411	4	US-09-517-739-2
4	17	1.0	423	1	US-08-470-179-189
5	17	1.0	1419	2	US-08-194-981E-4
6	17	1.0	1545	2	US-08-660-963-9
7	17	1.0	1576	3	US-09-101-146-63
8	17	1.0	1591	2	US-08-194-981E-3
9	17	1.0	1703	3	US-08-646-273-18
10	17	1.0	1852	1	US-08-201-118-10
11	17	1.0	1852	2	US-08-238-821B-10
12	17	1.0	1852	5	PCT-US95-05744-10
13	17	1.0	1854	1	US-08-201-118-4
14	17	1.0	1854	2	US-08-238-821B-4
15	17	1.0	1854	5	PCT-US95-05744-4
16	17	1.0	2129	3	US-08-646-273-22
17	17	1.0	2314	3	US-08-646-273-29
18	17	1.0	2707	2	US-08-709-874A-9
19	17	1.0	2707	4	US-09-104-382-9
20	17	1.0	2889	1	US-08-289-112-1
21	17	1.0	2907	2	US-09-018-628-17
22	17	1.0	2907	3	US-09-273-378-17
23	17	1.0	2907	4	US-09-018-635-26
24	17	1.0	2907	4	US-09-467-642-3
25	17	1.0	3697	1	US-08-571-758-1
26	17	1.0	3697	1	US-08-909-984A-1
27	17	1.0	3697	1	US-08-909-983-1

28	17	1.0	4127	4	US-09-487-368A-10	Sequence 10, Appl	
c	29	17	1.0	6453	1	US-08-306-691B-14	Sequence 14, Appl
30	17	1.0	6453	3	US-09-209-668-10	Sequence 10, Appl	
31	17	1.0	6453	3	US-09-356-952-8	Sequence 8, Appl	
32	17	1.0	9551	1	US-08-056-200-93	Sequence 93, Appl	
c	33	17	1.0	9551	2	US-08-800-644-93	Sequence 60, Appl
34	17	1.0	15652	4	US-09-422-936-60	Sequence 81, Appl	
35	17	1.0	28473	4	US-08-961-527-83	Sequence 3, Appl	
36	17	1.0	65042	4	US-09-784-316-3	Sequence 3, Appl	
37	17	1.0	84495	4	US-09-797-906-3	Sequence 3, Appl	
38	17	1.0	111282	4	US-09-754-250-3	Sequence 1, Appl	
c	39	17	1.0	4411529	4	US-09-103-840A-1	Sequence 1, Appl
40	16	1.0	21	3	US-08-784-551C-3	Sequence 3, Appl	
41	16	1.0	36	1	US-07-936-421-15	Sequence 15, Appl	
42	16	1.0	77	5	PCT-US95-10973A-19	Sequence 19, Appl	
43	16	1.0	146	3	US-08-765-340-9	Sequence 9, Appl	
44	16	1.0	239	1	US-08-248-474-47	Sequence 47, Appl	
45	16	1.0	239	3	US-08-756-849-47	Sequence 47, Appl	

ALIGNMENTS

RESULT 1
US-08-537-942A-2
; Sequence 2, Application US/08537942A
; Patent No. 5753464
; GENERAL INFORMATION:
; APPLICANT: HIRANO, TOSHIO
; APPLICANT: KAISHO, NISHINOMIYA
; TITLE OF INVENTION: GENE ENCODING A POLYPEPTIDE HAVING A
; TITLE OF INVENTION: PRE-B CELL GROWTH-SUPPORTING ABILITY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/537,942A
; FILING DATE: 21-NOV-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00819
; FILING DATE: 20-MAY-1994
; PRIOR APPLICATION DATA: JP 5-141178
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 4767-004-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1411 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1..84

; OTHER INFORMATION: /note= "IDENTIFICATION METHOD: E"
US-08-537-942A-2

Query Match 1.2%; Score 19; DB 1; Length 1411;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1112 ACAGCACCCTCTGACTG 1130

DB 948 ACAGCACCCTCTGACTG 966

RESULT 2

US-08-997-252A-2
; Sequence 2, Application US/08997252A
; Patent No. 6232453
; GENERAL INFORMATION:
; APPLICANT: HIRANO, TOSHIO
; APPLICANT: KAISHO, NISHINOMIYA
; TITLE OF INVENTION: GENE ENCODING A POLYPEPTIDE HAVING A
; PRE-B CELL GROWTH-SUPPORTING ABILITY
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,252A
; FILING DATE: 23-DEC-1997

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/537,942

; FILING DATE: 21-NOV-1995

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00819

; FILING DATE: 20-MAY-1994

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-141178

; FILING DATE: 21-MAY-1993

; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.

; REGISTRATION NUMBER: 24,618

; REFERENCE/DOCKET NUMBER: 4767-0005-0 PCT

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000

; TELEFAX: 703-413-2220

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1411 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA to mRNA

; FEATURE:

; NAME/KEY: sig_peptide

; LOCATION: 1..84

; OTHER INFORMATION: /note= "IDENTIFICATION METHOD: E"

US-08-997-252A-2

Query Match 1.2%; Score 19; DB 4; Length 1411;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1112 ACAGCACCCTCTGACTG 1130

DB 948 ACAGCACCCTCTGACTG 966

RESULT 3

US-09-517-739-2
; Sequence 2, Application US/09517739
; Patent No. 6307023
; GENERAL INFORMATION:
; APPLICANT: HIRANO, TOSHIO
; APPLICANT: KAISHO, NISHINOMIYA
; TITLE OF INVENTION: GENE ENCODING A POLYPEPTIDE HAVING A
; PRE-B CELL GROWTH-SUPPORTING ABILITY
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/517,739
; FILING DATE:

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,252

; FILING DATE: 23-DEC-1997

; APPLICATION NUMBER: US 08/537,942

; FILING DATE: 21-NOV-1995

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00819

; FILING DATE: 20-MAY-1994

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-141178

; FILING DATE: 21-MAY-1993

; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.

; REGISTRATION NUMBER: 24,618

; REFERENCE/DOCKET NUMBER: 4767-0005-0 PCT

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000

; TELEFAX: 703-413-2220

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1411 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA to mRNA

; FEATURE:

; NAME/KEY: sig_peptide

; LOCATION: 1..84

; OTHER INFORMATION: /note= "IDENTIFICATION METHOD: E"

US-09-517-739-2

Query Match 1.2%; Score 19; DB 4; Length 1411;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1112 ACAGCACCCTCTGACTG 1130

DB 948 ACAGCACCCTCTGACTG 966

RESULT 4

US-08-470-179-189/c

```
; Sequence 189, Application US/08470179
; Patent No. 5645994
; GENERAL INFORMATION:
; APPLICANT: Huang Ph.D, Wai Mun
; TITLE OF INVENTION: Method and Compositions for
; IDENTIFICATION OF SPECIES IN A SAMPLE
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Trask, Britt and Rossa
; STREET: P.O. Box 2550
; CITY: Salt Lake City
; STATE: Utah
; COUNTRY: USA
; ZIP: 84110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,179
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sweigert Ph.D, Susan E.
; REGISTRATION NUMBER: 36,289
; REFERENCE/DOCKET NUMBER: 2601
; TELEPHONE: 801-532-1922
; TELEFAX: 801-531-9168
; INFORMATION FOR SEQ ID NO: 189:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 423 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: not relevant
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Thermus thermophilus
; US-08-470-179-189

Query Match 1.0%; Score 17; DB 1; Length 423;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 48 GCAGGACCCCTTCCTGG 64
Db 61 GCAGGACCCCTTCCTGG 45

RESULT 5
US-08-194-981E-4
; Sequence 4, Application US/08194981E
; Patent No. 5886157
; GENERAL INFORMATION:
; APPLICANT: GUENGERICH, F. Peter
; APPLICANT: GUO, Zuyu
; APPLICANT: SANDHU, Punam
; APPLICANT: GILLAM, Elizabeth M. J.
; TITLE OF INVENTION: EXPRESSION AND PURIFICATION OF
; TITLE OF INVENTION: HUMAN
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street, NE
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1811
; COMPUTER READABLE FORM:
```

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,981E
; FILING DATE: February 10, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Selby
; REGISTRATION NUMBER: 38,298
; REFERENCE/DOCKET NUMBER: 22000.0022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 688-0770
; TELEFAX: (404) 688-9880
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1419 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-194-981E-4

Query Match 1.0%; Score 17; DB 2; Length 1419;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1266 GTGTGGGAGAGCCCTG 1282
Db 1250 GTGTGGGAGAGCCCTG 1266

RESULT 6
US-08-660-963-9
; Sequence 9, Application US/08660963
; Patent No. 5852187
; GENERAL INFORMATION:
; APPLICANT: Thorne, Michael O.
; APPLICANT: Gavlinn, Bruce D.
; APPLICANT: Horikawa, ReiKo
; APPLICANT: Lyons Jr., Charles E.
; TITLE OF INVENTION: MOLECULAR CLONING OF THE OVINE PITUITARY
; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE RECEPTOR
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: POPHAM, HAIK, SCHNOBRICH & KAUFMAN, LTD.
; STREET: Metropolitan Square Building, Suite 800, 1450
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,963
; FILING DATE: 12-JUN-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: O'Shaughnessy, Brian P.
; REGISTRATION NUMBER: 32,747
; REFERENCE/DOCKET NUMBER: 18046.036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-824-8000
; TELEFAX: 202-824-8199
; TELEX: 248516
; INFORMATION FOR SEQ ID NO: 9:
```

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1545 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: CDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..1371
US-08-660-963-9

Query Match 1.0%; Score 17; DB 2; Length 1545;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 484 GAGGCTGCTCCCTGTGCC 500
Db 478 GAGGCTGCTCCCTGTGCC 494

RESULT 7

US-09-101-146-63
; Sequence 63, Application US/09101146
; Patent No. 6124125
; GENERAL INFORMATION:
; APPLICANT: Dartmouth College, St. Vincents Institute of
; APPLICANT: Medical Research, Kemp et al.
; TITLE OF INVENTION: No. 6124125e1 AMP Activated Protein Kinase
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 66 E. Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053

COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PC
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/101.146
; FILING DATE: October 7, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PN7450
; FILING DATE: 8 JAN 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: DC-0050
; TELEPHONE: (856) 810-1515
; TELEFAX: (856) 810-1454
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1576
; TYPE: Nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: NO
US-09-101-146-63

Query Match 1.0%; Score 17; DB 3; Length 1576;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 737 ATGCTGACCATCACTGA 753
Db 346 ATGCTGACCATCACTGA 362

RESULT 8

US-08-194-981E-3
; Sequence 3, Application US/08194981E
; Patent No. 5886157
; GENERAL INFORMATION:
; APPLICANT: GUENGERICH, F. Peter
; APPLICANT: GUO, Zuyu
; APPLICANT: SANDHU, Punam
; APPLICANT: GILLAM, Elizabeth M. J.
; TITLE OF INVENTION: EXPRESSION AND PURIFICATION OF
; TITLE OF INVENTION: HUMAN
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street, NE
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,981E
; FILING DATE: February 10, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Selby
; REGISTRATION NUMBER: 38,298
; REFERENCE/DOCKET NUMBER: 22000.0022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 688-0770
; TELEFAX: (404) 688-9880
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1591 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-194-981E-3

Query Match 1.0%; Score 17; DB 2; Length 1591;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1266 GTGTGGGAGAGCCCTG 1282
Db 1304 GTGTGGGAGAGCCCTG 1320

RESULT 9

US-08-646-273-18
; Sequence 18, Application US/08646273
; Patent No. 6066502
; GENERAL INFORMATION:
; APPLICANT: Kroeger, Burkhard, Seulberger, Harald, Meyer, Thomas, Schmidt,
; APPLICANT: Martin, Jacob, Elard, Otter, Rainer, Subkowski, Thomas, Hillen, Hei
; TITLE OF INVENTION: Endothelin Converting Enzyme (ECE).
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Keil & Weinkauff
; STREET: 1101 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM AT-compatible, 80486 processor
; OPERATING SYSTEM: MS-DOS version 6.0
; SOFTWARE: WordPerfect version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646.273
; FILING DATE: 16-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/03706
; FILING DATE: 11-NOV-1994
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1703 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA for mRNA
US-08-646-273-18

Query Match 1.0%; Score 17; DB 3; Length 1703;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 647 CTGGAGATCAAGAGGC 663
Db 983 CTGGAGATCAAGAGGC 999

RESULT 10
US-08-201-118-10
; Sequence 10, Application US/08201118
; Patent No. 5786191
; GENERAL INFORMATION:
; APPLICANT: GOLDSTEIN, Joyce A.
; APPLICANT: ROMKES-SPARKS, Marjorie
; TITLE OF INVENTION: CLONING AND EXPRESSION OF COMPLEMENTARY
; TITLE OF INVENTION: DNAs FOR MULTIPLE MEMBERS OF THE HUMAN CYTOCHROME P450 2C
; TITLE OF INVENTION: SUBFAMILY
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/201.118
; FILING DATE: 22-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,962
; FILING DATE: 09-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 15280-192-1
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1852 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

US-08-201-118-10

Query Match 1.0%; Score 17; DB 1; Length 1852;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1266 GTGTGGGAGAGCCCTG 1282
Db 1314 GTGTGGGAGAGCCCTG 1330

RESULT 11
US-08-238-821B-10
; Sequence 10, Application US/08238821B
; Patent No. 5912120
; GENERAL INFORMATION:
; APPLICANT: GOLDSTEIN, Joyce A.
; APPLICANT: ROMKES-SPARKS, Marjorie
; APPLICANT: DE MORAIS, Sonia M.F.
; TITLE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN
; TITLE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT OF S-
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/238,821B
; FILING DATE: 06-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/201,118
; FILING DATE: 22-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,962
; FILING DATE: 09-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 15280-192110US
; TELEPHONE: (650) 326-2400
; TELEFAX: (650) 326-2422
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1852 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; NAME/KEY: Region
; LOCATION: 1..10
; OTHER INFORMATION: /note= "Corresponds to positions -10 to-1
; OTHER INFORMATION: for 65 of Figure 2."
US-08-238-821B-10

Query Match 1.0%; Score 17; DB 2; Length 1852;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1266 GTGTGGGAGAGCCCTG 1282
|||||

Db 1314 GTGTGGAGAGCCCTG 1330

RESULT 12

PCT-US95-05744-10

Sequence 10, Application PC/TUS9505744

GENERAL INFORMATION:

APPLICANT: GOLDSTEIN, Joyce A.

APPLICANT: ROMKES-SPARKS, Marjorie

APPLICANT: DE MORAIS, Sonia M.F.

TITLE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN

TITLE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT

TITLE OF INVENTION: OF S-MEPHNYTOIN METABOLISM

NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew

STREET: 379 Lytton Avenue

CITY: Palo Alto

STATE: California

COUNTRY: US

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/05744

FILING DATE: 06-MAY-1994

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/238,821

FILING DATE: 06-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/201,118

FILING DATE: 22-FEB-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/864,962

FILING DATE: 09-APR-1992

ATTORNEY/AGENT INFORMATION:

NAME: Dow, Karen B.

REGISTRATION NUMBER: 29,684

REFERENCE/DOCKET NUMBER: 15280-192-1-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 1852 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

PCT-US95-05744-10

Query Match 1.0%; Score 17; DB 5; Length 1852;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1266 GTGTGGAGAGCCCTG 1282

Db 1314 GTGTGGAGAGCCCTG 1330

RESULT 13

US-08-201-118-4

Sequence 4, Application US/08201118

Patent No. 5786191

GENERAL INFORMATION:

APPLICANT: GOLDSTEIN, Joyce A.

APPLICANT: ROMKES-SPARKS, Marjorie

TITLE OF INVENTION: CLONING AND EXPRESSION OF COMPLEMENTARY

TITLE OF INVENTION: DNAs FOR MULTIPLE MEMBERS OF THE HUMAN CYTOCHROME P450 2C

NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew

STREET: 379 Lytton Avenue

CITY: Palo Alto

STATE: California

COUNTRY: US

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/05744

FILING DATE: 06-MAY-1994

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/238,821

FILING DATE: 06-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/201,118

FILING DATE: 22-FEB-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/864,962

FILING DATE: 09-APR-1992

ATTORNEY/AGENT INFORMATION:

NAME: Dow, Karen B.

REGISTRATION NUMBER: 29,684

REFERENCE/DOCKET NUMBER: 15280-192-1-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 1852 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

PCT-US95-05744-10

Query Match 1.0%; Score 17; DB 5; Length 1852;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1266 GTGTGGAGAGCCCTG 1282

Db 1314 GTGTGGAGAGCCCTG 1330

RESULT 14

US-08-238-821B-4

Sequence 4, Application US/08238821B

Patent No. 5912120

GENERAL INFORMATION:

APPLICANT: GOLDSTEIN, Joyce A.

APPLICANT: ROMKES-SPARKS, Marjorie

APPLICANT: DE MORAIS, Sonia M.F.

TITLE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN

TITLE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT OF S-

TITLE OF INVENTION: MEPHENYTOIN METABOLISM

NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: US

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/238,821B

FILING DATE: 06-MAY-1994

Query Match 1.0%; Score 17; DB 1; Length 1854;

Best Local Similarity 100.0%; Pred. No. 1.1e-02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1266 GTGTGGAGAGCCCTG 1282

Db 1316 GTGTGGAGAGCCCTG 1332


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/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA: US 08/201,118
/ APPLICATION NUMBER:
/ FILING DATE: 22-FEB-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/864,962
/ FILING DATE: 09-APR-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Liebeschuetz, Joe
/ REGISTRATION NUMBER: 37,505
/ REFERENCE/DOCKET NUMBER: 15280-192110US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 326-2400
/ TELEFAX: (650) 326-2422
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1854 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 1..12
/ OTHER INFORMATION: /note= "Corresponds to positions -12 to-1
/ OTHER INFORMATION: for 25 of Figure 2."
US-08-238-821B-4

Query Match
Best Local Similarity 1.0%; Score 17; DB 2; Length 1854;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1266 GTGTGGGAGAGCCCTG 1282
| | | | | | | | | | | | | | | |
Db 1316 GTGTGGGAGAGCCCTG 1332

RESULT 15
PCT-US95-05744-4
/ Sequence 4, Application PC/TUS9505744
/ GENERAL INFORMATION:
/ APPLICANT: GOLDSTEIN, Joyce A.
/ APPLICANT: ROMKES-SPARKS, Marjorie
/ APPLICANT: DE MORAIS, Sonia M.F.
/ TITLE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN
/ TITLE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT
/ TITLE OF INVENTION: OF S-MEPHNYTOIN METABOLISM
/ NUMBER OF SEQUENCES: 61
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend Hourie and Crew
/ STREET: 379 Lytton Avenue
/ CITY: Palo Alto
/ STATE: California
/ COUNTRY: US
/ ZIP: 94301
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US95/05744
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/238,821
/ FILING DATE: 06-MAY-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/201,118
/ FILING DATE: 22-FEB-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/864,962
```

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/ FILING DATE: 09-APR-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Dow, Karen B.
/ REGISTRATION NUMBER: 29,684
/ REFERENCE/DOCKET NUMBER: 15280-192-1-1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 326-2400
/ TELEFAX: (415) 326-2422
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1854 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
PCT-US95-05744-4

Query Match
Best Local Similarity 1.0%; Score 17; DB 5; Length 1854;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1266 GTGTGGGAGAGCCCTG 1282
| | | | | | | | | | | | | | | |
Db 1316 GTGTGGGAGAGCCCTG 1332

Search completed: January 7, 2003, 20:22:20
Job time : 72.0864 secs
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According to the Pre Publication Rules, every patent application received by the United States Patent and Trademark Office after November 29, 2000 will be pre-published at eighteen months from the effective filing date. When the application is published the contents, including the sequences, will become prior art.

Two new databases have been created to hold the pre-published sequences:
Published_Applications_NA contains nucleic acid sequences; the search results will have the extension .rnpb.

Published_Applications_AA contains amino acid sequences; the search results will have the extension .rapb.

Each pre-published application is given a unique Publication Number. An example of a Publication Number is US20021234567A1. The "US" indicates the application was a U.S. application. The first 4 digits show the calendar year the application was published. The next 7 digits represent when the application was published. This 7-digit number starts at zero at the beginning of each calendar year. Each application published is given the next number in order. The "A" indicates a utility patent application and the "1" shows that this was the first time the application had been published. If the applicants submit changes to the application, they may request that the changed application be published again. In such instances, the "1" at the end of the number would be replaced by a "2".

Sequences in the PGPub database are public information; it is permissible to leave these results in the case.

;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 3373
;; LENGTH: 378
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC009974.3
;; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4
;; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.1
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4
;; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.9
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.8
;; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.8
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.3
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.8
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.4
US-09-864-761-3373

Query Match 20.1%; Score 346; DB 10; Length 378;
Best Local Similarity 100.0%; Pred. No. 4.2e-159;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGGCCCTCAGATCAAGAAGCCCTTCTTGCTCTGTGGCCCAACGGTGTGGGGCAGC 60
|||||
Db 362 CTTGGCCCTCAGATCAAGAAGCCCTTCTTGCTCTGTGGCCCAACGGTGTGGGGCAGC 303
QY 61 CCTCTATGGACAGCAAGACAGACTTTGTGGGTGAGGAGAGCTGGGAGGTGAAG 120
|||||
Db 302 CCTCTATGGACAGCAAGACAGACTTTGTGGGTGAGGAGAGCTGGGAGGTGAAG 243
QY 121 GGAGATGGAGAGGTGAGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGATAT 180
|||||
Db 242 GGAGATGGAGAGGTGAGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGATAT 183
QY 181 ACCACAAGCTTGGCTTCAGCCCAAGCCAGCCAGGGCCAGGGTGGAGAAAGTCCATCC 240
|||||
Db 182 ACCACAAGCTTGGCTTCAGCCCAAGCCAGCCAGGGCCAGGGTGGAGAAAGTCCATCC 123
QY 241 GGAGTCTGCATGGCCAGCTGGGAGACCCCTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 300
|||||
Db 122 GGAGTCTGCATGGCCAGCTGGGAGACCCCTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 63
QY 301 ATGACAGCTGACACCTTTTACCTCCGCTTACTGCATGGCCCTGTGC 346
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Db 62 ATGACAGCTGACACCTTTTACCTCCGCTTACTGCATGGCCCTGTGC 17

RESULT 3
US-09-826-581-5
; Sequence 5, Application US/09826581
; Patent No. US20020142310A1
; GENERAL INFORMATION:
; APPLICANT: Andersson, Leif
; APPLICANT: Luthman, U. Holger
; APPLICANT: Marklund, Stefan
; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT
; FILE REFERENCE: 11145-007001
; CURRENT APPLICATION NUMBER: US/09/826,581
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/195,665
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1647
; TYPE: DNA

;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (20)....(1486)
US-09-826-581-5

Query Match 9.8%; Score 168; DB 10; Length 1647;
Best Local Similarity 100.0%; Pred. No. 3.1e-72;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1523 GGTTCCTCTGTCGCCCGCCCTCTTCTCTACCGCACTATCCAAGATTTGGGCATCGC 1582
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Db 1022 GGTTCCTCTGTCGCCCGCCCTCTTCTCTACCGCACTATCCAAGATTTGGGCATCGC 1081
QY 1583 ACATTCCGAGACTTGGCTGTGGTGTGGACAGACAGCCCATCTGACTGACCTGGACATC 1642
|||||
Db 1082 ACATTCCGAGACTTGGCTGTGGTGTGGACAGACAGCCCATCTGACTGACCTGGACATC 1141
QY 1643 TTTGTGACCGCGGTGTGTCTGCACTGCCTGTGTCAACGAATGTGGT 1690
|||||
Db 1142 TTTGTGACCGCGGTGTGTCTGCACTGCCTGTGTCAACGAATGTGGT 1189

RESULT 4

US-09-864-761-20146/c
; Sequence 20146, Application US/09864761
; Patent No. US20020048763A1

;; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29

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; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 20146
; LENGTH: 92
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009974.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.8
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.4
; OTHER INFORMATION: NT HIT: g11430152, EVALUE 2.00e-22
; OTHER INFORMATION: EST_HUMAN HIT: BE327467.1, EVALUE 3.00e-06
; OTHER INFORMATION: SWISSPROT HIT: P54619, EVALUE 3.00e-03
US-09-864-761-20146
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Query Match 3.8%; Score 65; DB 10; Length 92;
Best Local Similarity 100.0%; Pred. No. 5.3e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 CCTGGCCCTCAGATCAAGAAGCCCTTCTTCTGCTGGGCCAACGGTGTGGGGCAGC 60
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Db 65 CCTGGCCCTCAGATCAAGAAGCCCTTCTTCTGCTGGGCCAACGGTGTGGGGCAGC 6
      |||||
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OY 61 CCCTC 65
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Db 5 CCCTC 1
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RESULT 5
US-09-864-761-27246
; Sequence 27246, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 27246
; LENGTH: 190
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004108.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.71
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.61
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.75
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.73
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.65
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.78
; OTHER INFORMATION: SWISSPROT HIT: P32595, EVALUE 7.60e-01
; OTHER INFORMATION: NT HIT: AF146793.2, EVALUE 4.40e-01
; OTHER INFORMATION: EST_HUMAN HIT: BE300286.1, EVALUE 1.70e-01
US-09-864-761-27246
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Query Match 1.1%; Score 19; DB 10; Length 190;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1232 CATCTCTGCAGCCTGTTTG 1250
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Db 90 CATCTCTGCAGCCTGTTTG 108
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RESULT 6
US-09-092-296-2/c
; Sequence 2, Application US/09092296
; Publication No. US20020188114A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/092,296
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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```
; APPLICATION NUMBER: 60/048,810
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6104.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 229 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-092-296-2

Query Match 1.1%; Score 19; DB 9; Length 229;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 TGAAGGAGATGGAGGAGG 134
Db 222 TGAAGGAGATGGAGGAGG 204

RESULT 7
US-09-092-296-1/c
; Sequence 1, Application US/09092296
; Publication No. US20020188114A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL USA
; COUNTRY: IL USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/092,296
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,810
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6104.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 base pairs
; TYPE: nucleic acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: base_polymorphism
; LOCATION: 200
; OTHER INFORMATION: /note= " N' represents an A or G or
; OTHER INFORMATION: T or C polymorphism at this position"
;
US-09-092-296-1

Query Match 1.1%; Score 19; DB 9; Length 239;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 TGAAGGAGATGGAGGAGG 134
Db 226 TGAAGGAGATGGAGGAGG 208

RESULT 8
US-09-092-296-5/c
; Sequence 5, Application US/09092296
; Publication No. US20020188114A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/092,296
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,810
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6104.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 389 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-092-296-5

Query Match 1.1%; Score 19; DB 9; Length 389;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 TGAAGGAGATGGAGGAGG 134
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Db 196 TGAAGGAGATGGAGG 178
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RESULT 9
US-09-092-296-6/c
; Sequence 6, Application US/09092296
; Publication No. US20020188114A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/092,296
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,810
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6104.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 413 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-092-296-6

Query Match 1.1%; Score 19; DB 9; Length 413;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 116 TGAAGGAGATGGAGG 134
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Db 223 TGAAGGAGATGGAGG 205
|||||
RESULT 10
US-09-992-598-362/c
; Sequence 362, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: KJavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 1.1%; Score 19; DB 9; Length 422;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 TGAAGGAGATGGAGGAGG 134
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Db 234 TGAAGGAGATGGAGGAGG 216

RESULT 11

US-09-989-293A-362/c
; Sequence 362, Application US/09989293A
; Patent No. US20020177164A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney,Austin L.
APPLICANT: Kljavin,Ivar J.
APPLICANT: Napier,Mary A.
APPLICANT: Pan,James
APPLICANT: Paoni,Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC66
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
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PRIOR APPLICATION NUMBER: 60/083322
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 1.1%; Score 19; DB 9; Length 422;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 116 TGAAGGAGATGGAGGAGG 134
Db 234 TGAAGGAGATGGAGGAGG 216

RESULT 12
US-10-063-547-65/c
; Sequence 65, Application US/10063547
; Publication No. US20020182638A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2230R1C1
; CURRENT APPLICATION NUMBER: US/10/063.547
; PRIOR FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 65
; LENGTH: 422
; TYPE: DNA

;
; ORGANISM: Homo Sapien
; US-10-063-547-65

Query Match 1.1%; Score 19; DB 9; Length 422;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 116 TGAAGGAGATGGAGGAGG 134
Db 234 TGAAGGAGATGGAGGAGG 216

RESULT 13
US-09-989-735-362/c
; Sequence 362, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: KJavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C61
; CURRENT APPLICATION NUMBER: US/09/989,735
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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RESULT 14
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; Sequence 362, Application US/09990444
; Publication No. US2002019300A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Klijavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PlC19
; CURRENT APPLICATION NUMBER: US/09/990,444
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR FILING DATE: 1997-11-24
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; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
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; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
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; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
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; PRIOR APPLICATION NUMBER: 60/090252
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; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
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; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 1.1%; Score 19; DB 9; Length 422;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 116 TGAAGGGAGATGGAGGAGG 134

Db 234 TGAAGGGAGATGGAGGAGG 216

RESULT 15

US-09-989-730-362/c

; Sequence 362, Application US/09989730
; Publication No. US20020197674A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC69
; CURRENT APPLICATION NUMBER: US/09/989,730
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR APPLICATION NUMBER: 60/087827
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; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 09:44:42 : Search time 2203.49 Seconds
(without alignments)
12656.598 Million cell updates/sec

Title: US-09-826-581-3
Perfect score: 1722
Sequence: 1 cctggccctcagatcaaga.....gatgagaggtcgggctgga 1722

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 15

Total number of hits satisfying chosen parameters: 56052

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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1: em_estba.*
2: em_esthum.*
3: em_estin.*
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6: em_estpl.*
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9: gb_est1.*
10: gb_est2.*
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12: gb_est3.*
13: gb_est4.*
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15: em_estfun.*
16: em_estom.*
17: gb_gss.*
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20: em_gss_pln.*
21: em_gss_vrt.*
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25: em_gss_other.*
26: em_gss_pro.*
27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	73	4.2	413	9 AA178898	AA178898 zp38d10.r
2	38	2.2	572	13 BI344527	BI344527 373008.MA
3	25	1.5	544	10 AW812866	AW812866 RC3-ST018
4	25	1.5	576	10 AW812884	AW812884 RC3-ST018
5	25	1.5	632	10 AW812763	AW812763 RC3-ST018
6	25	1.5	655	10 AW812747	AW812747 RC3-ST018

7	25	1.5	661	10	AW812746
8	24	1.4	458	17	AZ293182
9	24	1.4	461	10	BE126712
10	24	1.4	595	13	BM487789
11	24	1.4	636	12	BG711637
12	24	1.4	687	9	AJ451523
13	24	1.4	758	9	AJ396118
14	23	1.3	386	17	AQ926533
15	23	1.3	386	13	BI775360
16	22	1.3	258	10	BB538859
17	22	1.3	271	10	BB176083
18	22	1.3	660	17	B93026
19	22	1.3	799	17	AQ291862
20	21	1.2	180	9	AA250110
21	21	1.2	214	9	AI789929
22	21	1.2	219	10	BE667622
23	21	1.2	265	14	BQ569108
24	21	1.2	283	10	BE226658
25	21	1.2	286	10	BB527609
26	21	1.2	289	14	BQ570161
27	21	1.2	300	9	AA170921
28	21	1.2	308	10	BE667621
29	21	1.2	328	9	AV161169
30	21	1.2	333	12	BE848232
31	21	1.2	341	9	AA285611
32	21	1.2	345	9	AA981924
33	21	1.2	368	9	AA030629
34	21	1.2	368	12	BF149528
35	21	1.2	387	9	AA637403
36	21	1.2	396	9	AA444453
37	21	1.2	399	9	AA790002
38	21	1.2	399	14	W44300
39	21	1.2	400	9	AL364224
40	21	1.2	408	9	AA221662
41	21	1.2	411	12	BF780536
42	21	1.2	414	13	BI328511
43	21	1.2	417	10	BB687832
44	21	1.2	419	9	AU042711
45	21	1.2	419	9	AA271391

ALIGNMENTS

RESULT 1
AA178898
LOCUS
DEFINITION
zp38d10.r1 Stratagene muscle 937209 Homo sapiens cDNA clone
IMAGE:611731 5' similar to SW:AAKG_RAT_P80385 5'-AMP-ACTIVATED
PROTEIN KINASE, GAMMA CHAIN ;, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AA178898.1 GI:1760259
EST.
human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 413)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,

Kriznan, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin

J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,

White, Y., Wyllie, T., Waterston, R. and Wilson, R.

WashU-NCI human EST Project

Unpublished (1997)

Contact: Wilison RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: estowatson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1280 Std Error: 0.00

Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 255.

FEATURES

Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="GDB:4643570"
/db_xref="taxon:9606"
/clone_lib="IMAGE:611731"
/clone_lib="Stratagene muscle 937209"
/tissue_type="muscle"
/dev_stage="adult"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: skeletal muscle; Vector: pBluescript SK-;
Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally.
Primer: Oligo dt. Skeletal muscle from patient with
malignant hyperthermia. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; ~5 adaptor sequence: 5' GAATTCGGCAG
3' ~3' adaptor sequence: 5' CTCAGTTTTTTTTTTTTTTT 3'"

BASE COUNT 80 a 109 c 117 g 102 t 5 others

Query Match 4.2%; Score 73; DB 9; Length 413;
Best Local Similarity 100.0%; Pred. No. 2.8e-22;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1543 CTCCTCTCTACCGCACTATCCAGATTGGGCATCGGCACATTCGAGACTTGGCTGT 1602

Db 1 CTCCTCTCTACCGCACTATCCAGATTGGGCATCGGCACATTCGAGACTTGGCTGT 60

QY 1603 GGTGCTGGAGACA 1615

Db 61 GGTGCTGGAGACA 73

RESULT 2

BI344527 572 bp mRNA linear EST 30-JUL-2001

DEFINITION 373008 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.

ACCESSION BI344527

VERSION BI344527.1 GI:15037807

KEYWORDS EST.

SOURCE pig.

ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 572)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keale,J.W.

Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine

Unpublished (2000)

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCCTCAGTCAGACG

Plate: 119 row: I column: 11

Seq primer: ATTTAGGTGACACTATAG.

Location/Qualifiers
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FEATURES

source

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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 267 CCTGGGGTCAATTTCCCATCTCT 291

/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT 106 a 190 c 151 g 124 t 1 others

Query Match 2.2%; Score 38; DB 13; Length 572;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1562 ATCCAAGATTGGGCATCGGCACATTCGAGACTTGGC 1599

Db 223 ATCCAAGATTGGGCATCGGCACATTCGAGACTTGGC 260

RESULT 3

AW812866

LOCUS

DEFINITION RC3-ST0186-300100-017-b03 ST0186 Homo sapiens cDNA, mRNA sequence.

ACCESSION AW812866

VERSION AW812866.1 GI:7905860

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 544)

Dias Neto,E., Garcia Correa,R., Vertovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

CONTACT: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=RC3-ST0186-300

100-017-b03&t3=2000-01-30&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 33

High quality sequence stop: 542.

Location/Qualifiers

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/db_xref="taxon:9606"

/clone_lib="ST0186"

/dev_stage="Adult"

/note="Organ: stomach; Vector: puc18; Site 1: SmaI;

Site 2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

BASE COUNT 155 a 112 c 139 g 138 t

FEATURES

source

JOURNAL
MEDLINE
COMMENT

sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=RC3-ST0186-181
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High quality sequence stop: 636.
Location/Qualifiers

FEATURES

source

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/clone_lib="ST0186"
/dev_stage="Adult"

/note="Organ: stomach; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 179 a 146 c 159 g 171 t

ORIGIN

Query Match 1.5%; Score 25; DB 10; Length 655;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 267 CCTGGGCTCAATTCCCATCTGT 291
|||||
DB 447 CCTGGGCTCAATTCCCATCTGT 471

RESULT 7

AW812746

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AW812746 661 bp mRNA linear EST 17-MAY-2000
RC3-ST0186-181099-012-d10 ST0186 Homo sapiens cDNA, mRNA sequence.
AW812746
EST.
AW812746.1 GI:7905740

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 661)

REFERENCE

AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

Shogun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL

MEDLINE

COMMENT

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=RC3-ST0186-181
099-012-d10et3=1999-10-18&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence stop: 661.
Location/Qualifiers

FEATURES

source

1. .661
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0186"
/dev_stage="Adult"

/note="Organ: stomach; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 177 a 148 c 165 g 171 t

ORIGIN

Query Match 1.5%; Score 25; DB 10; Length 661;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 267 CCTGGGCTCAATTCCCATCTGT 291
|||||
DB 453 CCTGGGCTCAATTCCCATCTGT 477

RESULT 8

AZ293182

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 458)

Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret
B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
and Fraser, C.M.

Mouse BAC End Sequences from Library RPCI-23

Unpublished (1999)

Other GSSs: RPCI-23-159017-TV

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)

or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tldb/bacends/mouse/bac_end_intro.html

Plate: 159 row: O column: 17

Seq primer: SP6

Class: BAC ends.

Location/Qualifiers

1. .458

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-23-159017"

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/clone lib="RPCI-23"
/sex="Female"
/lab_host="DH108"
/notes="Organ: Kidney/Brain; Vector: pBACE3.6; Site 1:
EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methyase. Size
selected DNA was cloned into the pBACE3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH108 electrocompetent cells (BRL Life Technologies)."
BASE COUNT      142 a   74 c   117 g   125 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 GGGGAGGTGAAGGAGATGGAGGA 132
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DB 41 GGGGAGGTGAAGGAGATGGAGGA 64

RESULT 9
BE126712
LOCUS
DEFINITION
DEPA0460 Rat Lambda ZAP Express Library Rattus norvegicus cDNA 5',
mRNA sequence.
ACCESSION
BE126712
VERSION
BE126712.1 GI:8549403
KEYWORDS
SOURCE
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 461)
Sleeman,M.A., Murison,J.G., Strachan,L., Kumble,K.D., Glenn,M.P.,
McGrath,A., Grierson,A., Havukkala,I., Tan,P.L.J. and Watson,J.D.
Expressed sequence tags of cDNA clones from rat dermal papilla
cells
JOURNAL
Unpublished (2000)
COMMENT
Contact: Sleeman MA
Biology
Genesis Research and Development Corporation Limited
P.O. Box 50, 1 Fox St, Parnell, Auckland, New Zealand
Tel: 0064 9 373 5600
Fax: 0064 9 373 2189
Email: m.sleeman@genesis.co.nz
Seq primer: T3 forward
High quality sequence stop: 461.
FEATURES
source
Location/Qualifiers
1..461
/organism="Rattus norvegicus"
/strain="Dark-Agouti"
/db_xref="taxon:10116"
/clone_lib="Rat Lambda ZAP Express Library"
/tissue_type="vibrissae"
/cell_type="dermal papilla"
BASE COUNT      117 a   114 c   109 g   121 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 555 ATGCTGACCATCACTGACTTCATC 578
|||||
DB 246 ATGCTGACCATCACTGACTTCATC 269

RESULT 10
BM487789
LOCUS
DEFINITION
pgln.pk008.c13 Normalized Liver Library Gallus gallus cDNA clone
kinase, AMP-activated, gamma 1 non-catalytic subunit; AMPK gamma 1;
Protein kinase, AMP-activated, noncatalytic, gamma-1 [Homo sapiens]
gi|12737489 ref|XP_006778.2| protein kinase, AMP-activated, gamma 1
non, mRNA sequence.
ACCESSION
BG713637
VERSION
BG713637.1 GI:14007587
KEYWORDS
SOURCE
ORGANISM
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

```

```

DEFINITION
pgm2n.pk005.j24 Normalized Chicken Breast Muscle, Leg Muscle, and
Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA
clone pgm2n.pk005.j24 5' similar to gb|AAC52580.1 (U42413)
5'-AMP-activated protein kinase, gamma-1 subunit [Rattus norvegicus
], mRNA sequence.
ACCESSION
BM487789
VERSION
BM487789.1 GI:18608720
KEYWORDS
SOURCE
ORGANISM
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
REFERENCE
1 (bases 1 to 595)
AUTHORS
Cogburn,L.A. and Monsonego-Ornan,E.
TITLE
ESTs from Normalized Chicken Breast Muscle, Leg Muscle, and
Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal Genome
Project
JOURNAL
Unpublished (2002)
COMMENT
Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest.udel.edu.
FEATURES
source
Location/Qualifiers
1..595
/organism="Gallus gallus"
/strain="Commercial broiler and Ottawa Res. Centre
Strains 90 & 21"
/db_xref="taxon:9031"
/clone="pgm2n.pk005.j24"
/clone_lib="Normalized Chicken Breast Muscle, Leg Muscle,
and Epiphyseal Growth Plate cDNA library (pgm2n)"
/sex="Male and Female"
/tissue_type="Breast muscle, leg muscle and epiphyseal
growth plate"
/dev_stage="Breast;leg;Embryo(d19);post-hatch(1d,1.3,5,7,9
,11 weeks);growth plate(1d,7d,14d post-hatch)"
/lab_host="E. coli EMDH108"
/notes="Vector: pCMVSPORT6; Library made from equivalent
pools of total RNA isolated from each tissue (embryonic
muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth
plate 33.3% of the final RNA pool). Single pass sequencing
from 5'-end"
BASE COUNT      126 a   199 c   137 g   133 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 555 ATGCTGACCATCACTGACTTCATC 578
|||||
DB 146 ATGCTGACCATCACTGACTTCATC 169

RESULT 11
BG713637
LOCUS
DEFINITION
pgln.pk008.c13 Normalized Liver Library Gallus gallus cDNA clone
kinase, AMP-activated, gamma 1 non-catalytic subunit; AMPK gamma 1;
Protein kinase, AMP-activated, noncatalytic, gamma-1 [Homo sapiens]
gi|12737489 ref|XP_006778.2| protein kinase, AMP-activated, gamma 1
non, mRNA sequence.
ACCESSION
BG713637
VERSION
BG713637.1 GI:14007587
KEYWORDS
SOURCE
ORGANISM
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

```

QY 555 ATGCTGACCATCACTGACTTCATC 578
|||||

Fax: 301 838 0208
 Email: szhac@tigr.org
 Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieterdejong@med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics (http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html).
 Plate: 256 row: O column: 16
 Seq primer: SP6
 Class: BAC ends.

FEATURES

source
 Location/Qualifiers
 1..386
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-256O16"
 /clone_lib="RPCI-23"
 /sex="Female"
 /lab_host="DH10B"
 /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT 119 a 74 c 104 g 89 t
 ORIGIN

Query Match 1.3%; Score 23; DB 17; Length 386;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 110 GGGAGGTGAAGGAGATGGAGGA 132
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 Db 48 GGGAGGTGAAGGAGATGGAGGA 70

RESULT 15
 BI775360
 LOCUS BI775360 548 bp mRNA linear EST 25-SEP-2001
 DEFINITION 467815 MARC 280V Bos taurus cDNA 5', mRNA sequence.
 ACCESSION BI775360
 VERSION BI775360.1 GI:15776346
 KEYWORDS EST.
 SOURCE COW.

ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
 1 (bases 1 to 548)
 Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Perte, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
 JOURNAL Genome Res. 11 (4), 626-630 (2001)
 MEDLINE 21180013

COMMENT Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@mail.marc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
 PCR Primers

FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCCCGAGTCACGACG

Plate: 90 row: I column: 16
 Seq primer: ATTAGGTGACACTATAG.

FEATURES

source
 Location/Qualifiers
 1..548
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_lib="MARC 280V"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
 Library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

BASE COUNT 119 a 173 c 163 g 93 t
 ORIGIN

Query Match 1.3%; Score 23; DB 13; Length 548;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 CAGATCAAGAAGGCTTCTTTGC 33
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 Db 487 CAGATCAAGAAGGCTTCTTTGC 509

Search completed: January 6, 2003, 11:07:53
 Job time : 2212.49 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 20:16:02 ; Search time 64.9136 Seconds
(without alignments)
8135.386 Million cell updates/sec

Title: US-09-826-581-3
Perfect score: 1722
Sequence: 1 cctggccctccagatcaaga.....gatgagagctcggtgga 1722

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 15

Total number of hits satisfying chosen parameters: 989

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/prodata/2/ina/5A COMB.seq.*
2: /cgn2_6/prodata/2/ina/5B COMB.seq.*
3: /cgn2_6/prodata/2/ina/6A COMB.seq.*
4: /cgn2_6/prodata/2/ina/6B COMB.seq.*
5: /cgn2_6/prodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	24	1.4	11236	1	US-07-853-913-1
C 2	19	1.1	1411	1	US-08-537-942A-2
C 3	19	1.1	1411	4	US-08-997-252A-2
C 4	19	1.1	1411	4	US-09-517-739-2
C 5	19	1.1	2532	4	US-09-361-631-4
C 6	19	1.1	2993	4	US-09-361-631-3
C 7	19	1.1	40352	3	US-08-846-111D-15
C 8	19	1.1	40352	4	US-09-443-077-15
C 9	18	1.0	511	4	US-09-404-879A-68
C 10	18	1.0	740	4	US-09-342-681C-99
C 11	18	1.0	2838	4	US-08-246-489-1
C 12	18	1.0	3691	4	US-09-211-704A-3
C 13	18	1.0	3695	4	US-09-211-704A-1
C 14	18	1.0	5769	1	US-08-652-971-1
C 15	18	1.0	5769	2	US-08-991-258A-1
C 16	18	1.0	5769	2	US-08-769-399-1
C 17	18	1.0	5769	3	US-08-991-953A-1
C 18	18	1.0	9096	4	US-09-147-119-5
C 19	18	1.0	15936	4	US-09-147-119-1
C 20	17	1.0	495	1	US-08-215-805A-81
C 21	17	1.0	678	3	US-09-195-286-3
C 22	17	1.0	682	4	US-09-404-879A-52
C 23	17	1.0	692	4	US-09-404-879A-15
C 24	17	1.0	699	3	US-09-195-286-2
C 25	17	1.0	864	1	US-08-396-650-2
C 26	17	1.0	864	1	US-08-768-626-2
C 27	17	1.0	921	1	US-08-396-650-3

28 17 1.0 921 1 US-08-396-650-4 Sequence 4, Appli
29 17 1.0 921 1 US-08-768-626-3 Sequence 3, Appli
30 17 1.0 921 1 US-08-768-626-4 Sequence 4, Appli
C 31 17 1.0 1001 4 US-09-641-638-524 Sequence 524, App
C 32 17 1.0 1001 4 US-09-641-638-525 Sequence 525, App
C 33 17 1.0 1384 1 US-07-607-538C-1 Sequence 1, Appli
C 34 17 1.0 1384 2 US-08-162-402B-1 Sequence 1, Appli
35 17 1.0 1576 3 US-09-101-146-63 Sequence 63, Appli
36 17 1.0 1634 3 US-09-072-384-1 Sequence 1, Appli
37 17 1.0 1656 3 US-09-072-384-14 Sequence 14, Appli
38 17 1.0 1679 3 US-09-072-384-17 Sequence 17, Appli
C 39 17 1.0 1743 3 US-08-665-258-20 Sequence 20, Appli
C 40 17 1.0 1743 3 US-08-762-500-20 Sequence 20, Appli
C 41 17 1.0 1934 2 US-08-162-402B-7 Sequence 15, Appli
42 17 1.0 1937 3 US-08-888-949-15 Sequence 15, Appli
43 17 1.0 1937 4 US-08-888-950-15 Sequence 15, Appli
44 17 1.0 1937 4 US-09-262-758-15 Sequence 15, Appli
C 45 17 1.0 1974 3 US-08-762-500-78 Sequence 78, Appli

ALIGNMENTS

RESULT 1
US-07-853-913-1/c
; Sequence 1, Application US/07853913
; Patent No. 5338839
; GENERAL INFORMATION:
; APPLICANT: McKay, Ronald D.G.
; APPLICANT: Lendahl, Urban
; TITLE OF INVENTION: Nestin Expression As An Indicator of
; TITLE OF INVENTION: Neuroepithelial Tumors
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/853,913
FILING DATE: 19920319
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/660,412
FILING DATE: 22-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,803
FILING DATE: 25-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/201,762
FILING DATE: 02-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/180,548
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/POCKET NUMBER: MIT-4641AAAA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11236 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-07-853-913-1

Query Match 1.1%; Score 24; DB 1; Length 11236;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 975 CTCTTTCTGCAGAGTCTACCTGC 998
|||||
Db 7635 CTCTTTCTGCAGAGTCTACCTGC 7612

RESULT 2

US-08-537-942A-2
; Sequence 2, Application US/08537942A
; Patent No. 5753464
; GENERAL INFORMATION:
; APPLICANT: HIRANO, TOSHIO
; APPLICANT: KAISHO, NISHINOMIYA
; TITLE OF INVENTION: GENE ENCODING A POLYPEPTIDE HAVING A
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER& NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/537,942A
; FILING DATE: 21-NOV-1995

CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00819

FILING DATE: 20-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-141178

FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 4767-004-0 PCT

TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
; LENGTH: 1411 base pairs

TYPE: nucleic acid
; STRANDEDNESS: double

TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA

FEATURE:
; NAME/KEY: sig_peptide

LOCATION: 1..84
; OTHER INFORMATION: /note= "IDENTIFICATION METHOD: E"

US-08-537-942A-2

Query Match 1.1%; Score 19; DB 1; Length 1411;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1613 ACAGCACCCATCCTGACTG 1631
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Db 948 ACAGCACCCATCCTGACTG 966

RESULT 3

US-08-997-252A-2
; Sequence 2, Application US/08997252A
; Patent No. 6232453
; GENERAL INFORMATION:
; APPLICANT: HIRANO, TOSHIO
; APPLICANT: KAISHO, NISHINOMIYA
; TITLE OF INVENTION: GENE ENCODING A POLYPEPTIDE HAVING A
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER& NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,252A
; FILING DATE: 23-DEC-1997

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/537,942

FILING DATE: 21-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00819

FILING DATE: 20-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-141178

FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 4767-0005-0 PCT

TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
; LENGTH: 1411 base pairs

TYPE: nucleic acid
; STRANDEDNESS: double

TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA

FEATURE:
; NAME/KEY: sig_peptide

LOCATION: 1..84
; OTHER INFORMATION: /note= "IDENTIFICATION METHOD: E"

US-08-997-252A-2

Query Match

Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1613 ACAGCACCCATCCTGACTG 1631
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Db 948 ACAGCACCCATCCTGACTG 966

RESULT 4

US-09-517-739-2
; Sequence 2, Application US/09517739
; Patent No. 6307023
; GENERAL INFORMATION:
; APPLICANT: HIRANO, TOSHIO
; APPLICANT: KAISHO, NISHINOMIYA

;; TITLE OF INVENTION: GENE ENCODING A POLYPEPTIDE HAVING A
;; TITLE OF INVENTION: PRE-B CELL GROWTH-SUPPORTING ABILITY
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;; ADDRESSEE: P.C.
;; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
;; CITY: ARLINGTON
;; STATE: VA
;; COUNTRY: USA
;; ZIP: 22202
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/517,739
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/997,252
;; FILING DATE: 23-DEC-1997
;; APPLICATION NUMBER: US 08/537,942
;; FILING DATE: 21-NOV-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/JP94/00819
;; FILING DATE: 20-MAY-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 5-141178
;; FILING DATE: 21-MAY-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: OBLON, NORMAN F.
;; REGISTRATION NUMBER: 24,618
;; REFERENCE/DOCKET NUMBER: 4767-0005-0 PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703-413-3000
;; TELEFAX: 703-413-2220
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1411 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA to mRNA
;; FEATURE:
;; NAME/KEY: sig peptide
;; LOCATION: 1..84
;; OTHER INFORMATION: /note= "IDENTIFICATION METHOD: E"
;; US-09-517-739-2

Query Match 1.1%; Score 19; DB 4; Length 1411;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1613 ACAGCACCCTCTGACTG 1631
|||
Db 948 ACAGCACCCTCTGACTG 966

RESULT 5
US-09-361-631-4/c
; Sequence 4, Application US/09361631
; Patent No. 6383778
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Lindemeier, Juergen
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
; FILE REFERENCE: 02307E-08872005
; CURRENT APPLICATION NUMBER: US/09/361,631

;; CURRENT FILING DATE: 1999-07-27
;; EARLIER APPLICATION NUMBER: US 60/095,464
;; EARLIER FILING DATE: 1998-07-28
;; EARLIER APPLICATION NUMBER: US 60/112,747
;; EARLIER FILING DATE: 1998-12-17
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 4
;; LENGTH: 2532
;; TYPE: DNA
;; ORGANISM: Mus sp.
;; FEATURE:
;; OTHER INFORMATION: mouse G-protein coupled receptor (GPCR) B4
;; OTHER INFORMATION: nucleotide sequence
;; US-09-361-631-4

Query Match 1.1%; Score 19; DB 4; Length 2532;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 119 AGGAGATGGAGGAGTGA 137
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Db 2339 AGGAGATGGAGGAGTGA 2321

RESULT 6
US-09-361-631-3/c
; Sequence 3, Application US/09361631
; Patent No. 6383778
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Lindemeier, Juergen
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
; FILE REFERENCE: 02307E-08872005
; CURRENT APPLICATION NUMBER: US/09/361,631
; CURRENT FILING DATE: 1999-07-27
; EARLIER APPLICATION NUMBER: US 60/095,464
; EARLIER FILING DATE: 1998-07-28
; EARLIER APPLICATION NUMBER: US 60/112,747
; EARLIER FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2993
; TYPE: DNA
; ORGANISM: Rattus sp.
; FEATURE:
; OTHER INFORMATION: rat G-protein coupled receptor (GPCR) B4
; OTHER INFORMATION: nucleotide sequence
; US-09-361-631-3

Query Match 1.1%; Score 19; DB 4; Length 2993;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 119 AGGAGATGGAGGAGTGA 137
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Db 2351 AGGAGATGGAGGAGTGA 2333

RESULT 7
US-08-846-111D-15/c
; Sequence 15, Application US/08846111D
; Patent No. 6017705
; GENERAL INFORMATION:
; APPLICANT: Lurquin, Christophe; Brasseur, Francis;
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Are
; TITLE OF INVENTION: Members Of The Mage-B Family and Uses Thereof
; NUMBER OF SEQUENCES: 18

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;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022-7513
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect For DOS 6.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846.111D
; FILING DATE: 25-APRIL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/658,578
; FILING DATE: 5-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/403,388
; FILING DATE: 14-MARCH-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6017705man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5444.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40352 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-846-111D-15

Query Match 1.1%; Score 19; DB 3; Length 40352;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 468 GGCAGGGTGGGAGGGGAT 486
|||||
Db 14949 GGCAGGGTGGGAGGGGAT 14931

RESULT 8
US-09-443-077-15/c
; Sequence 15, Application US/09443077
; Patent No. 6392016
; GENERAL INFORMATION:
; APPLICANT: Lurquin, Christophe; Brasseur, Francis;
; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Are
; MEMBERS OF THE MAGE-8 FAMILY AND USES THEREOF
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022-7513
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect For DOS 6.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/443,077
; FILING DATE: 26-JUN-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,111
; FILING DATE: <Unknown>
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; APPLICATION NUMBER: 08/403,388
; FILING DATE: 14-MARCH-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6392016man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5444.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40352 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-443-077-15

Query Match 1.1%; Score 19; DB 4; Length 40352;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 468 GGCAGGGTGGGAGGGGAT 486
|||||
Db 14949 GGCAGGGTGGGAGGGGAT 14931

RESULT 9
US-09-404-879A-68
; Sequence 68, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 68
; LENGTH: 511
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-404-879A-68

Query Match 1.0%; Score 18; DB 4; Length 511;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 216 GCCCAGGGTGGGAGGAAAG 233
|||||
Db 248 GCCCAGGGTGGGAGGAAAG 265

RESULT 10
US-09-342-681C-99
; Sequence 99, Application US/09342681C
; Patent No. 6355782
; GENERAL INFORMATION:
; APPLICANT: Zonana et al.
; TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
; FILE REFERENCE: 52978
; CURRENT APPLICATION NUMBER: US/09/342,681C
; CURRENT FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/092,279
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/112,366
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 99
; LENGTH: 740
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-342-681C-99

Query Match 1.0%; Score 18; DB 4; Length 740;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 669 CCTCCTGGAGCCTGGTGC 686
Db 14 CCTCCTGGAGCCTGGTGC 31

RESULT 11

US-08-246-489-1/c
; Sequence 1, Application US/08246489
; Patent No. 6225049
; GENERAL INFORMATION:
; APPLICANT: Lan, Michael S.
; APPLICANT: No. 6225049kins, Abner L.
; TITLE OF INVENTION: NOVEL HUMAN INSULINOMA-ASSOCIATED cDNA
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobb, Martens, Olson & Bear
; STREET: 620 Newport Center Drive
; CITY: Newport Beach
; STATE: California
; COUNTRY: USA
; ZIP: 92660

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/246,489
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/901,715
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH012.012A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2838 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: IA-1

US-08-246-489-1

Query Match 1.0%; Score 18; DB 4; Length 2838;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 467 TGGCAGGTGGGAGGGG 484
Db 2544 TGGCAGGTGGGAGGGG 2527

RESULT 12

US-09-211-704A-3/c
; Sequence 3, Application US/09211704A
; Patent No. 6271014
; GENERAL INFORMATION:
; APPLICANT: de Saint-Vis, Blandine Marie
; APPLICANT: Fossiez, Francois
; APPLICANT: Caux, Christophe
; APPLICANT: Lebecque, Serge J.E.
; TITLE OF INVENTION: Mammalian Proteinases; Related Reagents
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/211,704A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/005,263
; FILING DATE: 09-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: SF0781K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3691 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 343..2028
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 406..2028
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3454
; OTHER INFORMATION: /note= "nucleotide 3454 designated W,
; OTHER INFORMATION: may be A or T."

US-09-211-704A-3

Query Match 1.0%; Score 18; DB 4; Length 3691;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 530 TCCTCCCGCCCTCCCC 547
Db 2389 TCCTCCCGCCCTCCCC 2372

RESULT 13

US-09-211-704A-1/c
; Sequence 1, Application US/09211704A
; Patent No. 6271014
; GENERAL INFORMATION:
; APPLICANT: de Saint-Vis, Blandine Marie
; APPLICANT: Fossiez, Francois

```
;
; APPLICANT: Caux, Christophe
; TITLE OF INVENTION: Mammalian Proteinases; Related Reagents
; TITLE OF INVENTION: and Methods
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/211.704A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/005,263
; FILING DATE: 09-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: SF0781K
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3695 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 344..2032
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 398..2032
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3458
; OTHER INFORMATION: /note= "nucleotide 3458 designated
; OTHER INFORMATION: W, may be A or T"
; US-09-211-704A-1
;
; Query Match 1.0%; Score 18; DB 4; Length 3695;
; Best Local Similarity 100.0%; Pred. No. 40;
; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 530 TCCTCCCGCCGCTCCCTCC 547
; DB 2393 TCCTCCCGCCGCTCCCTCC 2376
;
; RESULT 14
; US-08-652-971-1
; Sequence 1, Application US/08652971
; Patent No. 5814507
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd.
```

```
;
; CITY: South San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/652,971
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 225-3216
; TELEFAX: (415) 952-9881
; TELEX: 910 371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5769 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 379..4686
; US-08-652-971-1
;
; Query Match 1.0%; Score 18; DB 1; Length 5769;
; Best Local Similarity 100.0%; Pred. No. 39;
; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 274 CTCGAATTTCCCATCTGT 291
; DB 5612 CTCGAATTTCCCATCTGT 5629
;
; RESULT 15
; US-08-991-258A-1
; Sequence 1, Application US/08991258A
; Patent No. 5928887
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLBHR, HOHBACH, TEST, ALBRITTON & HERBERT, LLP
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/991.258A
; FILING DATE: 17-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/652,971
; FILING DATE: 24-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
```

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;
;   REGISTRATION NUMBER: 24,190
;   REFERENCE/DOCKET NUMBER: A-63478-3/WH/D/MTK
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 781-1989
;   TELEFAX: (415) 398-3249
;   TELEX:
;   INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 5769 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 379..4686
;   US-08-991-258A-1

Query Match      1.0%; Score 18; DB 2; Length 5769;
Best Local Similarity 100.0%; Pred. No. 39,
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 274 CTCAAATTTCCCATCTGT 291
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Db 5612 CTCAAATTTCCCATCTGT 5629
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Search completed: January 7, 2003, 20:22:10
Job time : 207.914 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 16:44:13 ; Search time 4127.03 Seconds
(without alignments)
11614.233 Million cell updates/sec

Title: US-09-826-581-5
Perfect score: 1647
Sequence: 1 ttggctctggggcggccaca.....acaccagcctcttagtcttc 1647

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

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- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
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- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1647	100.0	1647	6	AX281582	AX281582 Sequence
2	1372	83.3	2115	6	AX099802	AX099802 Sequence
3	1372	83.3	2115	9	AF214519	AF214519 Homo sapi
4	1366	82.9	2109	6	AX099776	AX099776 Sequence
5	1332	80.9	2290	9	HS2424977	AJ249977 Homo sapi
6	406	24.7	989	6	AX281579	AX281579 Sequence
7	285	17.3	206854	9	AC009974	AC009974 Homo sapi
8	278	16.9	1014	6	AX281581	AX281581 Sequence
9	278	16.9	152129	2	AC027416	AC027416 Homo sapi
10	197	12.0	152129	2	AC027416	AC027416 Homo sapi
11	168	10.2	1722	6	AX281580	AX281580 Sequence
12	57	3.5	106	11	G67375	G67375 A898 Human
13	52	3.2	821	6	AX281578	AX281578 Sequence
14	44	2.7	1867	6	AX099774	AX099774 Sequence
15	44	2.7	1873	4	AF214520	AF214520 Sus scro
16	44	2.7	1873	6	AX099800	AX099800 Sequence
17	44	2.7	1873	6	AX398331	AX398331 Sequence
18	44	2.7	1873	6	AX398333	AX398333 Sequence
19	44	2.7	1873	6	AX398335	AX398335 Sequence
20	44	2.7	1873	6	AX398337	AX398337 Sequence
21	44	2.7	1873	6	AX398339	AX398339 Sequence
22	44	2.7	2022	6	AX099804	AX099804 Sequence
23	38	2.3	5888	4	AF214521	AF214521 Sus scro
24	32	1.9	227724	2	AF336381	AF336381 Mus muscu
25	29	1.8	146577	2	AC128070	AC128070 Rattus no
26	29	1.8	190183	2	AC129703	AC129703 Rattus no
27	29	1.8	192968	2	AC127107	AC127107 Rattus no
28	29	1.8	192968	2	AC127107	AC127107 Rattus no
29	27	1.6	190183	2	AC129703	AC129703 Rattus no
30	24	1.5	1328	10	RNMPKXGAM	X95578 R.norvegicu
31	24	1.5	1550	10	RND42413	U42413 Rattus norv
32	23	1.4	808	6	AX398342	AX398342 Sequence
33	23	1.4	1095	6	AX398341	AX398341 Sequence
34	22	1.3	135394	10	AL672140	AL672140 Mouse DNA
35	22	1.3	246770	2	AC112790	AC112790 Mus muscu
36	21	1.3	24055	9	HSUC9A9	275743 Human DNA s
37	21	1.3	52780	9	AC026762	AC026762 Homo sapi
38	21	1.3	66341	2	AC118678	AC118678 Mus muscu
39	21	1.3	67674	2	AC101032	AC101032 Mus muscu
40	21	1.3	78184	9	AC067722	AC067722 Homo sapi
41	21	1.3	79414	2	AC023502	AC023502 Homo sapi
42	21	1.3	117362	2	AC094277	AC094277 Rattus no
43	21	1.3	123085	9	AL157406	AL157406 Human DNA
44	21	1.3	139619	2	AC074028	AC074028 Mus muscu
45	21	1.3	141415	2	AC008032	AC008032 Homo sapi

ALIGNMENTS

RESULT 1
AX281582
LOCUS AX281582 1647 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 5 from Patent WO0177305.
ACCESSION AX281582
VERSION AX281582.1 GI:16608833
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Andersson,L., Luthman,H. and Marklund,S.
TITLE Variants of the human amp-activated protein kinase gamma 3 subunit
JOURNAL Patent: WO 0177305-A 5 18-OCT-2001;

FEATURES	Araxis AB (SE)	Location/Qualifiers
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BASE COUNT	346 a	502 c 462 g 337 t
ORIGIN		
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	Best Local Similarity	100.0%; Pred. No. 0;
	Matches 1647; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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Db	1	TTGTGCTGGGCTGGCCACATGGAGCCCGGCTGGAGCAGCACTGGCGAGGACCCCTTC 60
Qy	61	CTGGAGCAGCCTTGGGGGTTCTGAGCATCAAGAGATGAGTCTCTTAGAGCAAGAAAAAG 120
Db	61	CTGGAGCAGCCTTGGGGGTTCTGAGCATCAAGAGATGAGTCTCTTAGAGCAAGAAAAAG 120
Qy	121	CAGCTCATGGCCATCACACAGCTGTGACCAGCAGCTCAGAAAGATCCGTGGGAACCGAG 180
Db	121	CAGCTCATGGCCATCACACAGCTGTGACCAGCAGCTCAGAAAGATCCGTGGGAACCGAG 180
Qy	181	GGCCAAAGCCTTGAGATGGACAAGCGAGAAGTCTGGTGGAGGAAGGGAGCCACAGGTCA 240
Db	181	GGCCAAAGCCTTGAGATGGACAAGCGAGAAGTCTGGTGGAGGAAGGGAGCCACAGGTCA 240
Qy	241	GGGGGAAGGTCCTGGTCCAGGCCAGTGTGATGTCCACCGGGCTGGAGGCCACATTCCC 300
Db	241	GGGGGAAGGTCCTGGTCCAGGCCAGTGTGATGTCCACCGGGCTGGAGGCCACATTCCC 300
Qy	301	CAAGACACACCTTGGCTCAAGCTGATCTCTCGCGGGTGGGCACTCCACACAGGGTG 360
Db	301	CAAGACACACCTTGGCTCAAGCTGATCTCTCGCGGGTGGGCACTCCACACAGGGTG 360
Qy	361	GGATGCTCCCTCTCTGACTGTACAGCTCAGCTGTCAGGGTCTCCAGCAGATGATGGGA 420
Db	361	GGATGCTCCCTCTCTGACTGTACAGCTCAGCTGTCAGGGTCTCCAGCAGATGATGGGA 420
Qy	421	GCTGGCCACGAGTTCCAGCCAAGAGGCTGGGAGTGTGAGCTAGAAGGCCCTGCTGGA 480
Db	421	GCTGGCCACGAGTTCCAGCCAAGAGGCTGGGAGTGTGAGCTAGAAGGCCCTGCTGGA 480
Qy	481	AGAGAGGCTGCCCTGTGCTGTCCCGCAGGCCCCATTCCCAAGCTGGGCTGGGATGA 540
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Db	541	CGAACTGCGGAAACCCCGCGCCAGATCTACATCGCGCTTCATGCAGGAGCACACCTGCTA 600
Qy	601	CGATGCCATGCAACTAGCTCCAAAGCTAGTCACTTCGACACCATGCTGGAGATCAAGAA 660
Db	601	CGATGCCATGCAACTAGCTCCAAAGCTAGTCACTTCGACACCATGCTGGAGATCAAGAA 660
Qy	661	GGCCTCTTTGCTCTGGTGGCCAAAGGTGTGCGGGAGCCCCCTCTATGGGACAGCAAGAA 720
Db	661	GGCCTCTTTGCTCTGGTGGCCAAAGGTGTGCGGGAGCCCCCTCTATGGGACAGCAAGAA 720

QY	721	GCAGAGCTTTGTGGGGATGCTGACCACTCACTGACTTCATCTCTGGTGCTGCATCGCTACTA	780
DB	721	GCAGAGCTTTGTGGGGATGCTGACCACTCACTGACTTCATCTCTGGTGCTGCATCGCTACTA	780
QY	781	CAGGTCCCCCTGGTCAGAGTCTATGAGATTGAAACAATAAGATTGACACCTGGAGGGA	840
DB	781	CAGGTCCCCCTGGTCAGAGTCTATGAGATTGAAACAATAAGATTGACACCTGGAGGGA	840
QY	841	GATCTACTGTAAGGCTGCTTCAAGGCTCTGGTCTCCATCTCTCCCTAATGATAGCCTGTT	900
DB	841	GATCTACTGTAAGGCTGCTTCAAGGCTCTGGTCTCCATCTCTCCCTAATGATAGCCTGTT	900
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DB	901	TGAAGCTGTCTACACCTCATCAAGAACCGGATCCATCGCTGCCCTGTTCTTTGACCCGGT	960
QY	961	GTCAAGCAAGTACTCCACATCTCACACACAAAGCCCTGCTCAAGTTTCTGCACATCTT	1020
DB	961	GTCAAGCAAGTACTCCACATCTCACACACAAAGCCCTGCTCAAGTTTCTGCACATCTT	1020
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DB	1021	TGGTTCCCTGCTGCCCGGCCCTCTCTTCTTCTTACCGCACTATCCAAGATTTTGGGCATCGG	1080
QY	1081	CACATTCCGAGACTTGGCTGTGGTGCTGAGACAGGACCCCATCTGACTGCACTGGACAT	1140
DB	1081	CACATTCCGAGACTTGGCTGTGGTGCTGAGACAGGACCCCATCTGACTGCACTGGACAT	1140
QY	1141	CTTTGTGGACCGGCGTGTCTGTCACTGCTGTGGTCAACGAATCTGGTCAGGTGCTGGG	1200
DB	1141	CTTTGTGGACCGGCGTGTCTGTCACTGCTGTGGTCAACGAATCTGGTCAGGTGCTGGG	1200
QY	1201	CCTCTATTCCCGCTTTGATGTGATTCACCTGCTGCCCGAGCAAACTCAACACCACTGGA	1260
DB	1201	CCTCTATTCCCGCTTTGATGTGATTCACCTGCTGCCCGAGCAAACTCAACACCACTGGA	1260
QY	1261	CATGAGTGTGGGAGAACCTCTGAGCAGAGGACACTATGTCTGGAGGGAGTCCCTTCCCTG	1320
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DB	1321	CCAGCCCCACGAGAGCTTGGGGGAAGTGTATCGACAGGATTTGCTCGGGAGCAGGTACACAG	1380
QY	1381	GCTGGTGTAGTGGACGAGACCCAGCATCTCTTTGGGCGTGTCTCCCTCTCCGACATCCT	1440
DB	1381	GCTGGTGTAGTGGACGAGACCCAGCATCTCTTTGGGCGTGTCTCCCTCTCCGACATCCT	1440
QY	1441	TCAGGCACTGGTGTCTCAGCCCTGCTGGCATCGATGCCCTCGGGGCTGAGAAGATCTGAG	1500
DB	1441	TCAGGCACTGGTGTCTCAGCCCTGCTGGCATCGATGCCCTCGGGGCTGAGAAGATCTGAG	1500
QY	1501	TCCTCAATCCCAAGCCACCTGCACACCTGGAAGCCAAATGAAGGGAACCTGGAGAACCTCAGC	1560
DB	1501	TCCTCAATCCCAAGCCACCTGCACACCTGGAAGCCAAATGAAGGGAACCTGGAGAACCTCAGC	1560
QY	1561	CTTCACTTTCCCCCAGCCCAATTTGCTGGTTACGCTATGATTACAGGTAGGCTCTGCCCTG	1620
DB	1561	CTTCACTTTCCCCCAGCCCAATTTGCTGGTTACGCTATGATTACAGGTAGGCTCTGCCCTG	1620
QY	1621	GGCCATGACACAGGCTCTTAGTCTTC 1647	
DB	1621	GGCCATGACACAGGCTCTTAGTCTTC 1647	
RESULT 2			
AX099802			
LOCUS	AX099802	2115 bp	DNA linear PAT 02-APR-
DEFINITION	Sequence 29 from Patent WO0120003.		
ACCESSION	AX099802		
VERSION	AX099802.1 GI:13538836		
KEYWORDS			

LOCUS	AX099802	2115 bp	DNA	linear	PAT 02-APR-2001
DEFINITION	Sequence 29 from Patent WO0120003.				
ACCESSION	AX099802				
VERSION	AX099802.1	GI:13538836			
KEYWORDS					

SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	1 (bases 1 to 2115) Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Anderson, L., Looft, C., Kalm, E., Milan, D., Robic, A., Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and Chardon, P.
TITLE	Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof
JOURNAL	Patent: WO 0120003-A 29 22-MAR-2001; INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ; Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)
FEATURES	Location/Qualifiers
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BASE COUNT	460 a 622 c 562 g 471 t
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Query Match 83.3%; Score 1372; DB 6; Length 2115; Best Local Similarity 99.9%; Pred. No. 0; Matches 1422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	95 ATGAGCTTCCTAGACACAGAAAACAGCAGCTCATGGCCATCACAGCTGTGACCAGCAGC 154
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Qy	155 TCAGAAAGAAATCCGTGGGAAACGGAGGCCAAAGCCTTTGAGATGGACAGCAGCAAGTCG 214
Db	61 TCAGAAAGAAATCCGTGGGAAACGGAGGCCAAAGCCTTTGAGATGGACAGCAGCAAGTCG 120
Qy	215 GTGAGGAAAGGGAGCCACACAGGTGAGGGGAAGGTCCCGGTCCAGGCCAGCTGCTGAG 274
Db	121 GTGAGGAAAGGGAGCCACACAGGTGAGGGGAAGGTCCCGGTCCAGGCCAACTGCTGAG 180
Qy	275 TCCACCGGCTGGAGGCCACATTCCCAAGACCAACACCTTTGGCTCAAGCTGATCTGACC 334
Db	181 TCCACCGGCTGGAGGCCACATTCCCAAGACCAACACCTTTGGCTCAAGCTGATCTGACC 240
Qy	335 GGGGTGGGCACTCCACCAACAGGTGGGACTGCCTCCCTCTGACTGTACAGCCTCAGCT 394
Db	241 GGGGTGGGCACTCCACCAACAGGTGGGACTGCCTCCCTCTGACTGTACAGCCTCAGCT 300
Qy	395 GCAAGCTCCAGCACAGATGATGTGGAGCTGGCCACGGAGTTCCAGCCACACAGAGCCCTGG 454
Db	301 GCAAGCTCCAGCACAGATGATGTGGAGCTGGCCACGGAGTTCCAGCCACACAGAGCCCTGG 360
Qy	455 GAGTGTGAGCTAGAGGCTCTCTGGAAGAGAGGCTGCCCTGTGCTGTCTCCCGCAGGCC 514
Db	361 GAGTGTGAGCTAGAGGCTCTCTGGAAGAGAGGCTGCCCTGTGCTGTCTCCCGCAGGCC 420
Qy	515 CCATTTCCCAAGCTGGGCTGGGATGACAACTGCGGAAACCCGCGCCAGCTACATG 574
Db	421 CCATTTCCCAAGCTGGGCTGGGATGACAACTGCGGAAACCCGCGCCAGCTACATG 480
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Db	601 GCAGCCCTCTATGGGACACAGAGAGAGCTTTGTGGGGATGCTGACCATCACTGAC 660
Qy	755 TTCACTCTGCTGCTGCTATCGCTACTACAGGTCCCCCTGCTCCAGATCTATGAGATTGAA 814
Db	661 TTCACTCTGCTGCTGCTATCGCTACTACAGGTCCCCCTGCTCCAGATCTATGAGATTGAA 720
Qy	815 CAACATTAAGATTGAGACTCGAGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGCTC 874
Db	721 CAACATTAAGATTGAGACTCGAGGAGATCTACCTGCAAGGCTGCTTCAAGCCTCTGCTC 780
Qy	875 TCCATCTCTCTAATGATAGCTGTTTGAAGCTGTCTACACCTCATCAAGAACCAGGATC 934
Db	781 TCCATCTCTCTAATGATAGCTGTTTGAAGCTGTCTACACCTCATCAAGAACCAGGATC 840
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Qy	995 CGCTGCTCAAGTTCTGTCACATCTTTGGTTCCCTGCTGCCCGGCCCTCTCTCTCTAC 1054
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Qy	1055 CGCACTATCAAGATTGGGCATCGGCACATTCGGAGACTTGGCTGTGGTGGGAGACA 1114
Db	961 CGCACTATCAAGATTGGGCATCGGCACATTCGGAGACTTGGCTGTGGTGGGAGACA 1020
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Qy	1235 GCCCAGCAACCTTACACCACTGGACATGAGTGTGGGAGAGCCCTGAGGCAAGGACA 1294
Db	1141 GCCCAGCAACCTTACACCACTGGACATGAGTGTGGGAGAGCCCTGAGGCAAGGACA 1200
Qy	1295 CTATGCTGGAGGAGTCTCTTTCTCCAGCCCAAGAGCTTTGGGGAAAGTATGATCGAC 1354
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Qy	1355 AGGATTGCTCGGAGCAGGTATACAGGCTGGTGTCTAGTGGACGAGACCCAGCATCTCTTG 1414
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Qy	1415 GCGTGTGCTCTCCCTCTCCGACATCTTACGGCACTGGTGTCTAGCCCTGCTGGCATCGAT 1474
Db	1321 GCGTGTGCTCTCCCTCTCCGACATCTTACGGCACTGGTGTCTAGCCCTGCTGGCATCGAT 1380
Qy	1475 GCCTCGGGGCTTGAGAAGATCTGAGTCTCAATCCCAAGCCA 1517
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RESULT 3	AF214519	2115 bp	mRNA	linear	PRI 03-JUN-2000
LOCUS	AF214519				
DEFINITION	Homo sapiens AMP-activated protein kinase gamma subunit (PRKAG3)				
ACCESSION	AF214519				
VERSION	AF214519.1	GI:8215681			
KEYWORDS					
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				

REFERENCE AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 2115) Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A., Thelander, M., Rogel-Gaillard, C., Paul, S., Iannuccelli, N., Raak, L., Ronne, H., Lundstrom, K., Reinsch, N., Gellin, J., Kaim, E., Roy, P.L., Chardon, P. and Andersson, L. A mutation in PRKAG3 associated with excess glycogen content in pig skeletal muscle Science 288 (5469), 1248-1251 (2000) 20280150 10818001
TITLE	2. (bases 1 to 2115) Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A., Rogel-Gaillard, C., Paul, S., Gellin, J., Lundstrom, K., Reinsch, N., Kaim, E., Le Roy, P., Chardon, P. and Andersson, L. Direct Submission Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC box 597, Uppsala 751 24, Sweden
FEATURES source	Location/Qualifiers 1..2115 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="2" /map="2p" /tissue type="skeletal muscle" 1..2115 /gene="PRKAG3" 1..1395 /gene="PRKAG3" /note="AMPK3" /codon_start=1 /product="AMP-activated protein kinase gamma subunit" /protein_id="AAF3987.1" /db_xref="GI:8215682" /translation="MSFLEQENSSWSPAVTSSSRIRGKRRAKALRWTRQKSVBEG EPQGGGPRPRFAETAGLEATFPKTTPLAQADPAVGTPPTGWDCLPSDCTASAG SSTDVDELATEFPAETAMECELELEERFALCLSPQAPFKLWDDDLRKPQAQIYM RFMOHCTCDAMATSSKLVIFDTMLEIKKAPFALVANGVRAAPLWDSKQSFVGMILT TDFILVHRVYRSPLOIYEIOHKIETWREIYLOGKFLVLSISPNDSLPEAVYTLI KNRTHRLPVLDPVSNVLIHLTHKRLKFLHGLSLPRPSFLRYRTQDILGIGTFRDL AVULETPIALTALDIFVDRRVSAIPVNEGVVGLYSRFDVILHAAQQTNYNHLNWSV GEAUKRTLCLEGLVSCOPHESLGEVIDRIAREQVHRLVLVDVETQHLGLGVVSUDILQ ALVLSPAIGDALGA"
gene	460 a 622 c 562 g 471 t
CDS	
BASE COUNT ORIGIN	
Query Match	83.3%; Score 1372; DB 9; Length 2115;
Best Local Similarity	99.9%; Pred. No. 0;
Matches 1422; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
Qy	95 ATGAGCTTCCTAGACAAAGAAAACAGCAGCTCATGCCCATCACCAGCTGTGACCAAGCAGC 154
Db	1 ATGAGCTTCCTAGACAAAGAAAACAGCAGCTCATGCCCATCACCAGCTGTGACCAAGCAGC 60
Qy	155 TCAGAAAGAAATCCGTGGGAAACGGAGGSCCAAAGCCTTTGAGATGACCAAGGCAAGTCG 214
Db	61 TCAGAAAGAAATCCGTGGGAAACGGAGGSCCAAAGCCTTTGAGATGACCAAGGCAAGTCG 120
Qy	215 GTGAGGAGGAGGAGCCACAGCTCAGGGGAGAGTCCCGGTCAGGCCAGCTGCTGAG 274
Db	121 GTGAGGAGGAGGAGCCACAGCTCAGGGGAGAGTCCCGGTCAGGCCAGCTGCTGAG 180
Qy	275 TCCACCGGGCTGGAGGCCACATTCCTCCCAAGACCAACCTTTGGCTCAAGCTGATCCTGCC 334
Db	181 TCCACCGGGCTGGAGGCCACATTCCTCCCAAGACCAACCTTTGGCTCAAGCTGATCCTGCC 240
Qy	335 GGGTGGGCACTTCACCAACAGGTTGGGCACTGCCCTCCCTCTGACTGTACAGCTCAGCT 394
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Db	301 GCAGGCTCCAGCAGACAGATGATGTGGAGCTGGCCACAGGAGTTCCACAGCCACAGAGGCTCTGG 360
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Db	361 GAGTGTAGCTAGAGGCTCTGTGGAAGAGAGGCTCTCCCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 420
Qy	515 CCATTTCCCAAGCTGGGCTGGGATGACGAATCTGGGAAACCCGGGCAACCCGAGATCTACATG 574
Db	421 CCATTTCCCAAGCTGGGCTGGGATGACGAATCTGGGAAACCCGGGCAACCCGAGATCTACATG 480
Qy	575 CGCTTATGTCAGGAGCAGCACCTGCTACGATGCCATGCCATGCCATGCCATGCCATGCCATGCCATGCC 634
Db	481 CGCTTATGTCAGGAGCAGCACCTGCTACGATGCCATGCCATGCCATGCCATGCCATGCCATGCCATGCC 540
Qy	635 TTGACACACCTGCTGGAGATCAAGAAGGCTCTTTGCTCTGCTGGTGGCAACGGTGTGCGG 694
Db	541 TTGACACACCTGCTGGAGATCAAGAAGGCTCTTTGCTCTGCTGGTGGCAACGGTGTGCGG 600
Qy	695 GCAGCCCTCTATGGGACAGCAAGACAGAGCTTTGTGGGATGCTGACCATCAGCTGAC 754
Db	601 GCAGCCCTCTATGGGACAGCAAGACAGAGCTTTGTGGGATGCTGACCATCAGCTGAC 660
Qy	755 TTGATCTGCTGCTGATCGCTACTACAGTCCCTGCTCCAGATCTATGAGATTGAA 814
Db	661 TTGATCTGCTGCTGATCGCTACTACAGTCCCTGCTCCAGATCTATGAGATTGAA 720
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ACCESSION AJ249977
VERSION AJ249977.1 GI:6688200
KEYWORDS AMP-activated protein kinase; AMPK gamma 3 gene; gamma 3 subunit.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2290)
AUTHORS Cheung, P.C., Salt, I.P., Davies, S.P., Hardie, D.G. and Carling, D.
TITLE Characterization of AMP-activated protein kinase gamma-subunit isoforms and their role in AMP binding
JOURNAL Biochem. J. 346 Pt 3, 659-669 (2000)
MEDLINE 20164049
PUBMED 10698692
REFERENCE 2 (bases 1 to 2290)
AUTHORS Carling, D.
TITLE Direct Submission
JOURNAL Submitted (12-OCT-1999) Carling D., Cellular Stress Group, MRC Clinical Sciences Centre, Hammersmith Hospital, DuCane Road, London, W12 0NN, UNITED KINGDOM
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DEFINITION	Sequence 2 from Patent WO0177305.		
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VERSION	AX281579.1	GI:16608830	
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REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 Anderson,L., Luthman,H. and Marklund,S.		
TITLE	Variants of the human amp-activated protein kinase gamma 3 subunit		
JOURNAL	Patent: WO 0177305-A 2 18-OCT-2001;		
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Tateno, M., Catanesi, J. J., and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this clone is at base position 1 of RP11-459119; actual end is at base position 206854 of RP11-459119.

Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 and AC009974. A single plasmid region exists between 38812-38903. An unresolved tandem in the HERV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing.

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DEFINITION Sequence 4 from Patent WO0177305.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
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AUTHORS Anderson, L., Luthman, H. and Marklund, S.
TITLE Variants of the human amp-activated protein kinase gamma 3 subunit
JOURNAL Patent: WO 0177305-A 4 18-OCT-2001;
AREXIS AB (SE)
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DEFINITION Homo sapiens clone RP11-504G11, WORKING DRAFT SEQUENCE, 32
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ACCESSION AC027416
VERSION AC027416.2 GI:8317289
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AUTHORS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-504G11
Unpublished
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bada, P.,
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Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tefaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.
Direct Submission
Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 7, 2000 this sequence version replaced gi:7342115.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L7458
Center clone name: 504.G.11
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 135376 bases at least Q40
Consensus quality: 143264 bases at least Q30
Consensus quality: 146503 bases at least Q20
Insert size: 161000; agarose-fp
Insert size: 149029; sum-of-contigs
Quality coverage: 3.1 in Q20 bases; agarose-fp
Quality coverage: 3.3 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 32 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1005: contig of 1005 bp in length
* 1006 1105: gap of 100 bp
* 1106 2402: contig of 1297 bp in length
* 2403 2502: gap of 100 bp
* 2503 3823: contig of 1321 bp in length
* 3824 3923: gap of 100 bp
* 3924 5020: contig of 1097 bp in length
* 5021 5120: gap of 100 bp
* 5121 6161: contig of 1041 bp in length
* 6162 6261: gap of 100 bp
* 6262 7547: contig of 1286 bp in length

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* 7548 7647: gap of 100 bp
* 7648 9983: contig of 2336 bp in length
* 9984 10083: gap of 100 bp
* 10084 12556: contig of 2473 bp in length
* 12557 12656: gap of 100 bp
* 12657 15043: contig of 2387 bp in length
* 15044 15143: gap of 100 bp
* 15144 17123: contig of 1980 bp in length
* 17124 17223: gap of 100 bp
* 17224 19466: contig of 2243 bp in length
* 19467 19566: gap of 100 bp
* 19567 21928: contig of 2362 bp in length
* 21929 22028: gap of 100 bp
* 22029 24319: contig of 2291 bp in length
* 24320 24419: gap of 100 bp
* 24420 27059: contig of 2640 bp in length
* 27060 27159: gap of 100 bp
* 27160 30170: contig of 3011 bp in length
* 30171 30270: gap of 100 bp
* 30271 33968: contig of 3698 bp in length
* 33969 34069: gap of 100 bp
* 34069 38179: contig of 4111 bp in length
* 38180 38279: gap of 100 bp
* 38280 42366: contig of 4087 bp in length
* 42367 42466: gap of 100 bp
* 42467 46365: contig of 3899 bp in length
* 46366 46466: gap of 100 bp
* 46466 51285: contig of 4820 bp in length
* 51286 51385: gap of 100 bp
* 51386 55871: contig of 4486 bp in length
* 55872 55971: gap of 100 bp
* 55972 60595: contig of 4624 bp in length
* 60596 60695: gap of 100 bp
* 60696 66595: contig of 5900 bp in length
* 66596 66695: gap of 100 bp
* 66696 73218: contig of 6523 bp in length
* 73219 73318: gap of 100 bp
* 73319 77115: contig of 3797 bp in length
* 77116 77215: gap of 100 bp
* 77216 85023: contig of 7807 bp in length
* 85023 85123: gap of 100 bp
* 85123 93415: contig of 8192 bp in length
* 93415 101193: contig of 7779 bp in length
* 101194 101294: gap of 100 bp
* 101294 113090: contig of 11797 bp in length
* 113091 113190: gap of 100 bp
* 113191 123496: contig of 10306 bp in length
* 123497 123596: gap of 100 bp
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* 137838 137937: gap of 100 bp
* 137938 152129: contig of 14192 bp in length.
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FEATURES

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1106..2402
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2503..3823
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5121..6161
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Best Local Similarity 100.0%; Pred. No. 9.2e-137; Indels 0; Gaps 0;

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QY 1370 CAGGTACACAGGCTGGTGTAGTGGACGAGACCCAGCATCTCTTGGGCGTGTCTCCCTC 1429
Db 139718 CAGGTACACAGGCTGGTGTAGTGGACGAGACCCAGCATCTCTTGGGCGTGTCTCCCTC 139777
QY 1430 TCCGACATCTTCAGGCACTGGTGCTCAGCCCTGCTGGCATCGATCCCTCGGGGCTTGA 1489
Db 139778 TCCGACATCTTCAGGCACTGGTGCTCAGCCCTGCTGGCATCGATCCCTCGGGGCTTGA 139837
QY 1490 GAAGATCTGAGTCTCTCAATCCCAAGCCACCTGCACACCTGGAAGCCAAATGAAGGAACTG 1549
Db 139838 GAAGATCTGAGTCTCTCAATCCCAAGCCACCTGCACACCTGGAAGCCAAATGAAGGAACTG 139897
QY 1550 GAGAACTCAGCCTTCATCTTCCCCACCCCATTTGCTGGTTTCAGCTATGATTCAGGTAG 1609
Db 139898 GAGAACTCAGCCTTCATCTTCCCCACCCCATTTGCTGGTTTCAGCTATGATTCAGGTAG 139957
QY 1610 GCTCTGCCCTGGGCCATGACACAGCCTCTTAGTCTTC 1647
Db 139958 GCTCTGCCCTGGGCCATGACACAGCCTCTTAGTCTTC 139995
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RESULT 10
AC027416/c

LOCUS	AC027416	152129 bp	DNA	linear	HTG 07-JUN-2000
DEFINITION	Homo sapiens clone RP11-504G11, WORKING DRAFT SEQUENCE, 32 unordered pieces.				
ACCESSION	AC027416				
VERSION	AC027416.2	GI:8317289			
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.				
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 152129)				
AUTHORS	Birren,B., Linton,L., Nusbaum,C. and Lander,E.				
TITLE	Homo sapiens, clone RP11-504G11				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 152129)				
AUTHORS	Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Laroque,K., Lanazares,R., Landers,T., Lehoczyk,J., Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meltrin,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N., Piesani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.				
TITLE	Direct Submission				
JOURNAL	Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA				
COMMENT	On Jun 7, 2000 this sequence version replaced gi:7342115. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html				
	----- Genome Center -----				
	Center: Whitehead Institute/ MIT Center for Genome Research				
	Center code: WIBR				
	Web site: http://www-seq.wi.mit.edu				
	Contact: sequence.submissions@genome.wi.mit.edu				
	----- Project Information -----				
	Center project name: L7458				
	Center clone name: 504_G_11				
	----- Summary Statistics -----				
	Sequencing vector: M13; M77815; 100% of reads				
	Chemistry: Dye-terminator Big Dye; 100% of reads				
	Assembly program: Phrap; version 0.960731				
	Consensus quality: 135376 bases at least Q40				
	Consensus quality: 143284 bases at least Q30				
	Consensus quality: 146503 bases at least Q20				
	Insert size: 161000; agarose-1p				
	Insert size: 149029; sum-of-contigs				
	Quality coverage: 3.1 in Q20 bases; agarose-1p				
	Quality coverage: 3.3 in Q20 bases; sum-of-contigs				

	** NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.				
	1 1005: contig of 1005 bp in length				
	1006 1105: gap of 100 bp				

	FEATURES				
	Location/Qualifiers				
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	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	/clone="RP11-504G11"				
	/clone_lib="RPC1-11 Human Male BAC"				
	1. .1005				
	/note="assembly_fragment"				
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	1106. .2402				
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	2503. .3823				
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	1106 2402: contig of 1297 bp in length				
	2403 2502: gap of 100 bp				
	2503 3823: contig of 1321 bp in length				
	3824 3923: gap of 100 bp				
	3924 5020: contig of 1097 bp in length				
	5021 5120: gap of 100 bp				
	5121 6161: contig of 1041 bp in length				
	6162 6261: gap of 100 bp				
	6262 7547: contig of 1286 bp in length				
	7548 7647: gap of 100 bp				
	7648 9983: contig of 2336 bp in length				
	9984 10083: gap of 100 bp				
	10084 12556: contig of 2473 bp in length				
	12557 12656: gap of 100 bp				
	12657 15043: contig of 2387 bp in length				
	15044 15143: gap of 100 bp				
	15144 17123: contig of 1980 bp in length				
	17124 17223: gap of 100 bp				
	17224 19466: contig of 2243 bp in length				
	19467 19566: gap of 100 bp				
	19567 21928: contig of 2362 bp in length				
	21929 22028: gap of 100 bp				
	22029 24319: contig of 2291 bp in length				
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	24420 27059: contig of 2640 bp in length				
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	27160 30170: contig of 3011 bp in length				
	30171 30270: gap of 100 bp				
	30271 33968: contig of 3698 bp in length				
	33969 34068: gap of 100 bp				
	34069 38179: contig of 4111 bp in length				
	38180 38279: gap of 100 bp				
	38280 42366: contig of 4087 bp in length				
	42367 42466: gap of 100 bp				
	42467 46365: contig of 3899 bp in length				
	46366 46465: gap of 100 bp				
	46466 51285: contig of 4820 bp in length				
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	51386 55871: contig of 4486 bp in length				
	55872 55971: gap of 100 bp				
	55972 60595: contig of 4624 bp in length				
	60596 60695: gap of 100 bp				
	60696 66595: contig of 5900 bp in length				
	66596 66695: gap of 100 bp				
	66696 73218: contig of 6523 bp in length				
	73219 73318: gap of 100 bp				
	73319 77115: contig of 3797 bp in length				
	77116 77215: gap of 100 bp</				

Denaturation: 94 degrees C for 30 seconds
Annealing: 55 degrees C for 30 seconds
Polymerization: 72 degrees C for 30 seconds
PCR cycles: 33
Thermal cycler: Perkin Elmer 9600
Protocol:

Template: 25 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Taq Polymerase: 0.1 units/reaction
Total Vol: 15 ul

Buffer:

MgCl2: 2 mM
KCl: 50 mM
Tris-HCL: 20 mM
pH: 8.4

Primers were defined on sequence AA178898 (cDNA). No intron.

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Location/Qualifiers
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/db_xref="taxon:9606"
/clone_lib="Human"
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BASE COUNT
ORIGIN
1. .18

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Best Local Similarity 100.0%; Pred. No. 2.9e-18;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 13
AX281578
LOCUS
DEFINITION
Sequence 1 from Patent WO0177305.
ACCESSION
AX281578
VERSION
AX281578.1 GI:16608829
KEYWORDS
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1
AUTHORS
Andersson, L., Luchman, H. and Marklund, S.
TITLE
Variants of the human amp-activated protein kinase gamma 3 subunit
JOURNAL
Patent: WO 0177305-A 1 18-OCT-2001;
Arexis AB (SE)

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Location/Qualifiers
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/db_xref="taxon:9606"
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Query Match 3.2%; Score 52; DB 6; Length 821;
Best Local Similarity 100.0%; Pred. No. 8.6e-16;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 313 TTGGTCTGGGCTGGCCACATGAGCCGGCTGGAGCAGCAGCTGGCAGG 364

RESULT 14
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LOCUS
DEFINITION
Sequence 1 from Patent WO0120003.
ACCESSION
AX099774
VERSION
AX099774.1 GI:13538808
KEYWORDS
SOURCE
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ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

DEFINITION
ACCESSION
AX099774
VERSION
AX099774.1 GI:13538808
KEYWORDS
SOURCE
pig.
ORGANISM
Sus scrofa

REFERENCE
1
AUTHORS
Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A.,
Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., Le Roy, P. and
Chardon, P.

TITLE
Variants of the gamma chain of ampk, dna sequences encoding the
same, and uses thereof
JOURNAL
Patent: WO 0120003-A 1 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ;
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm, Ernst (DE)

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BASE COUNT
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RESULT 15
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DEFINITION
Sus scrofa AMP-activated protein kinase gamma subunit (PRKAG3)
mRNA, complete cds.
ACCESSION
AF214520
VERSION
AF214520.1 GI:8215683
KEYWORDS
SOURCE
Sus scrofa.

ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE
1
AUTHORS
Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A., Thelander, M.,
Rogel-Gaillard, C., Paul, S., Iannuccelli, N., Raak, L., Ronne, H.,
Lundstrom, K., Reinsch, N., Gellin, J., Kalm, E., Roy, P.L., Chardon, P.
and Andersson, L.

TITLE
A mutation in PRKAG3 associated with excess glycogen content in pig
skeletal muscle
JOURNAL
Science 288 (5469), 1248-1251 (2000)

MEDLINE
20280150
PUBMED
10818001
REFERENCE
2
AUTHORS
Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A.,
Rogel-Gaillard, C., Paul, S., Gellin, J., Lundstrom, K., Reinsch, N.,
Kalm, E., Le Roy, P., Chardon, P. and Andersson, L.

TITLE
Direct Submission
JOURNAL
Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish
University of Agricultural Sciences, BMC box 597, Uppsala 751 24,

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BASE COUNT          382 a 580 c 535 g 376 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 535 GTCATCTTCGACACATCGCTCGAGATCAAGAGCGCTTCTTTC 578
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Search completed: January 7, 2003, 20:19:51
Job time : 4648.03 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 09:44:41 ; Search time 314.832 Seconds
(without alignments)
11781.028 Million cell updates/sec

Title: US-09-826-581-5
Perfect score 1647
Sequence: 1 ttggctggggctggccaca.....acaccagctcttagcttc 1647

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 15

Total number of hits satisfying chosen parameters: 6064

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 20: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
- 21: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
- 22: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
- 23: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
- 24: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1647	100.0	1647	22	AAH43685 PRKAG3 CDNA. Homo
2	1372	83.3	2115	22	AAD03320 Human AMPK gamma s
3	1366	82.9	2109	22	AAD03296 Human AMPK gamma s
4	406	24.7	989	22	AAH43682 PRKAG3 intron 2 -
5	398	24.2	547	22	ABA08485 Human AMP-activate
6	278	16.9	1014	22	AAH43684 PRKAG3 intron 10 -
7	252	15.3	3425	22	AAK72740 Human immune/haema
8	252	15.3	3425	22	AAK72741 Human immune/haema
9	168	10.2	1722	22	AAH43683 PRKAG3 intron 4 -

C	10	85	5.2	378	22	ABA44706	Human breast cell
C	11	85	5.2	378	22	ABA55162	Human foetal liver
C	12	85	5.2	378	22	ABA24907	Probe #3373 for ge
C	13	85	5.2	378	22	AAK03423	Human brain expres
C	14	85	5.2	378	22	AAK28874	Human bone marrow
C	15	85	5.2	378	22	AAI13465	Probe #3398 for ge
C	16	85	5.2	378	22	AAI13465	Probe #3398 for ge
C	17	85	5.2	378	22	AAI03344	Probe #3335 used t
C	18	85	5.2	378	22	AAI03344	Probe #3335 used t
C	19	54	3.3	378	24	ABS03407	Human genome-deriv
C	20	54	3.3	378	24	ABA49850	Human breast cell
C	21	54	3.3	378	22	ABA67769	Human foetal liver
C	22	54	3.3	378	22	ABA34826	Probe #13292 for g
C	23	54	3.3	378	22	AAK16181	Human brain expres
C	24	54	3.3	378	22	AAK41922	Human bone marrow
C	25	54	3.3	378	22	AAI22692	Probe #12625 for g
C	26	54	3.3	378	22	AAI47988	Probe #16674 used t
C	27	54	3.3	378	22	AAI08354	Probe #8345 used t
C	28	52	3.2	821	22	ABS15953	Human genome-deriv
C	29	44	2.7	1867	22	AAH43681	PRKAG3 5'untranscr
C	30	44	2.7	1873	22	AAD03319	Pig AMPK gamma sub
C	31	44	2.7	1873	22	AAD03319	Pig AMPK gamma sub
C	32	44	2.7	1873	24	AAD36456	Pig wild-type PRKA
C	33	44	2.7	1873	24	AAD36457	Pig PRKAG3 polymor
C	34	44	2.7	1873	24	AAD36458	Pig PRKAG3 polymor
C	35	44	2.7	1873	24	AAD36459	Pig PRKAG3 polymor
C	36	44	2.7	1873	24	AAD36460	Pig PRKAG3 polymor
C	37	23	1.4	2022	22	AAD03321	Sub scrofa PRKAG3
C	38	23	1.4	2022	22	AAH43695	PRKAG3 reverse pri
C	39	23	1.4	808	24	AAD36462	Pig PRKAG3 gene 5'
C	40	20	1.2	1095	24	AAD36461	Pig PRKAG3 gene 5'
C	41	20	1.2	333	24	ABK74111	Bacillus lichenifo
C	42	19	1.2	3385	24	AAD22073	Dermacentor melano
C	43	19	1.2	21	24	AAD36471	Pig PRKAG3 gene co
C	44	19	1.2	22	24	AAD36463	Pig PRKAG3 gene co
C	45	19	1.2	23	24	AAD36468	Pig PRKAG3 gene co
C	45	19	1.2	510	21	AAC75342	Human ORFX ORF897

ALIGNMENTS

RESULT 1
AAH43685
ID AAH43685 standard; cDNA; 1647 BP.
XX
AC AAH43685;
DT 21-JAN-2002 (first entry)
XX
DE PRKAG3 CDNA.
XX
KW Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
metabolic disease; diabetes; obesity; substitution; ss.
XX
OS Homo sapiens.
XX
FH Key
CDS Location/Qualifiers
20..1489
/tag= a
/product= "PRKAG3"
230
/tag= b
/label= "C230G"
559
/note= "Causes P71A"
/tag= c
/label= "T559C"
/note= "Silent variation"
1037
/tag= d
/label= "C1037T"
/note= "Causes R340W"

PN W0200177305-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-SE00765.
XX 07-APR-2000; 2000US-195665P.
XX (AREX-) AREXIS AB.
XX Andersson L, Luthman H, Marklund S;
XX WPI; 2001-657170/75.
DR P-PSDB; QQB47679.
XX
XX New variants of human AMP-activated protein kinase gamma3 subunit
PT associated with a metabolic disease e.g. diabetes or obesity and method
PT for determining a risk estimate of diseases in subject by detecting the
PT variant -
XX
PS Disclosure; Fig 5; 25pp; English.
XX
XX This sequence represents the full length cDNA encoding the human
CC AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting
CC the presence of the PRKAG3 DNA, or a variant, is useful in determining
CC a risk estimate of a metabolic disease, such as diabetes or obesity,
CC in a subject. The variation may occur in exons 3, 4 or 10. In exon
CC 3 variation may be a substitution of a G for a C at nucleotide 320,
CC resulting in the amino acid substitution P71A; in exon 4 variation may
CC be a substitution of a T for a C at nucleotide 550; and in exon 10
CC variation may be a substitution of a T for a C at nucleotide 1037,
CC resulting in the amino acid substitution R340W. There may also be
CC nucleotide variation in intron 6. The numbering of these
CC variations is based on the full length cDNA as given, rather than on
CC position 1 of the open reading frame.
XX
SQ Sequence 1647 BP; 346 A; 502 C; 462 G; 337 T; 0 other;

Query March 100.0%; Score 1647; DB 22; Length 1647;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 1647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGTCTGGGCTGGCCACATGGAGCCGGCTGGAGCAGCACTGGCAGGACCCCTTC 60
Db 1 TTGGTCTGGGCTGGCCACATGGAGCCGGCTGGAGCAGCACTGGCAGGACCCCTTC 60

Qy 61 CTGAGCAGCCTTGGGGTCTTGAGCATCAAGAGATGAGCTTCTAGAGCAAGAAACAG 120
Db 61 CTGAGCAGCCTTGGGGTCTTGAGCATCAAGAGATGAGCTTCTAGAGCAAGAAACAG 120

Qy 121 CAGCTCATGGCCATCACAGCTGTGACCAAGCTGAGCAAGAAATCCGTGGGAAACGGAG 180
Db 121 CAGCTCATGGCCATCACAGCTGTGAGCAAGCTGAGCAAGAAATCCGTGGGAAACGGAG 180

Qy 181 GGCCAAAGCCTTGAGATGGCAAGGCAAGAGTCCGTGGAGGAAGGAGCCACAGGTC 240
Db 181 GGCCAAAGCCTTGAGATGGCAAGGCAAGAGTCCGTGGAGGAAGGAGCCACAGGTC 240

Qy 241 GGGGGAAGGTCCTGGTCCAGGCAGCTGTGAGTCCACCGGGCTGGAGCCACATTC 300
Db 241 GGGGGAAGGTCCTGGTCCAGGCAGCTGTGAGTCCACCGGGCTGGAGCCACATTC 300

Qy 301 CAAGACCACACCTTGGCTCAAGCTGATCTGCGGGGTGGGCACTCCACCAAGAGG 360
Db 301 CAAGACCACACCTTGGCTCAAGCTGATCTGCGGGGTGGGCACTCCACCAAGAGG 360

Qy 361 GGACTGCTCCCTCTGACTGTACAGCCTCAGCTGAGGCTCCAGCAGAGATGATG 420
Db 361 GGACTGCTCCCTCTGACTGTACAGCCTCAGCTGAGGCTCCAGCAGAGATGATG 420

Qy 421 GCTGGCCACAGGATTCACAGCCTCAGCTGAGGCTGGAGCTGAGAGGCTGCTGGA 480
Db 421 GCTGGCCACAGGATTCACAGCCTCAGCTGAGGCTGGAGCTGAGAGGCTGCTGGA 480

Qy 481 AGAGAGGCTGCTGCTGTGCTGTCCCGAGGCCCATTTCCCAAGCTGGGCTGGATGA 540
Db 481 AGAGAGGCTGCTGCTGTGCTGTCCCGAGGCCCATTTCCCAAGCTGGGCTGGATGA 540

Qy 541 CGAACTGCGGAAACCCGGCGCCAGATCTACATGCGCTTTCATGCAAGGACACCTGCTA 600
Db 541 CGAACTGCGGAAACCCGGCGCCAGATCTACATGCGCTTTCATGCAAGGACACCTGCTA 600

Qy 601 CGATGCGCATGGCAACTAGCTCCAAGCTAGTCTTCCACACCATGCTGGAGATCAAGAA 660
Db 601 CGATGCGCATGGCAACTAGCTCCAAGCTAGTCTTCCACACCATGCTGGAGATCAAGAA 660

Qy 661 GGCCTTCTTGTGCTGTGGTGGCCAAACGGTGTGCGGCGAGCCCTCTATGGGACACAGAA 720
Db 661 GGCCTTCTTGTGCTGTGGTGGCCAAACGGTGTGCGGCGAGCCCTCTATGGGACACAGAA 720

Qy 721 GCAGAGCTTTGTGGGATGCTGACCATCAGTCTCATCTGGTGTGCTGCTACTA 780
Db 721 GCAGAGCTTTGTGGGATGCTGACCATCAGTCTCATCTGGTGTGCTGCTACTA 780

Qy 781 CAGGTCCCTGCTGCTCAGATCTATGAGATTCAACACATAGATTGAGACCTGGAGGA 840
Db 781 CAGGTCCCTGCTGCTCAGATCTATGAGATTGAACACATAGATTGAGACCTGGAGGA 840

Qy 841 GATCTACCTGCAAGCTGCTTCAAGCCTCTGGTCTCCATCTCTCTAATGATAGCTGTT 900
Db 841 GATCTACCTGCAAGCTGCTTCAAGCCTCTGGTCTCCATCTCTCTAATGATAGCTGTT 900

Qy 901 TGAAGCTGTCTACACCTCTCATCAAGAACCGGATCCATCGGCTGCTGCTTCTTGAACCGGT 960
Db 901 TGAAGCTGTCTACACCTCTCATCAAGAACCGGATCCATCGGCTGCTGCTTCTTGAACCGGT 960

Qy 961 GTGAGGCAACGTATCCACATCTCACACAAACGGCTCTCAAGTTCCTGCAACATCTT 1020
Db 961 GTGAGGCAACGTATCCACATCTCACACAAACGGCTCTCAAGTTCCTGCAACATCTT 1020

Qy 1021 TGGTTCCTGCTGCTGCGGCCCTCTTCTCTACCGCACTATCAAGATTGGGCACTGG 1080
Db 1021 TGGTTCCTGCTGCTGCGGCCCTCTTCTCTACCGCACTATCAAGATTGGGCACTGG 1080

Qy 1081 CACATTCGAGACTTGGCTGTGGTGTGGAGACAGACCCATCTCTGACTGCACTGGACAT 1140
Db 1081 CACATTCGAGACTTGGCTGTGGTGTGGAGACAGACCCATCTCTGACTGCACTGGACAT 1140

Qy 1141 CTTTGTGGAACGGGCTGTGCTGCACTGCTGGTCAACGAAATGTTGGTCAAGTTCCTGGG 1200
Db 1141 CTTTGTGGAACGGGCTGTGCTGCACTGCTGGTCAACGAAATGTTGGTCAAGTTCCTGGG 1200

Qy 1201 CCTCTATTCCCGCTTTGATGATGATTCACCTGGCTGCGGCAAGAACCTACAAACCTGGA 1260
Db 1201 CCTCTATTCCCGCTTTGATGATGATTCACCTGGCTGCGGCAAGAACCTACAAACCTGGA 1260

Qy 1261 CATGAGTGTGGGAAGCCCTGAGGAGAGGACACTATGTCTGGAGGGAGTCTCTTCCTG 1320
Db 1261 CATGAGTGTGGGAAGCCCTGAGGAGAGGACACTATGTCTGGAGGGAGTCTCTTCCTG 1320

Qy 1321 CCAGCCCCACAGAGCTTGGGGAAGTGTGACAGGATGCTCGGGAGCAGGTACACAG 1380
Db 1321 CCAGCCCCACAGAGCTTGGGGAAGTGTGACAGGATGCTCGGGAGCAGGTACACAG 1380

Qy 1381 GCTGGTGTAGTGGAGAGCCAGCATCTCTTGGGCGTGGTCTCCCTCTCCGACATCT 1440
Db 1381 GCTGGTGTAGTGGAGAGCCAGCATCTCTTGGGCGTGGTCTCCCTCTCCGACATCT 1440

Qy 1441 TCAGGCACTGGTGTCTCAGCCCTGCTGGCATCGATGCTCGGGGCTGAGAAAGATCTGAG 1500
Db 1441 TCAGGCACTGGTGTCTCAGCCCTGCTGGCATCGATGCTCGGGGCTGAGAAAGATCTGAG 1500

Qy 1501 TCCTCAATCCCAAGCCACCTGGACACCTGGAAAGCCAATGAAGGGAACTGGAGAACTCAGC 1560
Db 1501 TCCTCAATCCCAAGCCACCTGGACACCTGGAAAGCCAATGAAGGGAACTGGAGAACTCAGC 1560

QY 1561 CTTTCATCTTCCCCACCCCATTTGCTGGTTTCAGCTATGATTCAGGTAGGCTGCGCTG 1620
Db |||||||
QY 1561 CTTTCATCTTCCCCACCCCATTTGCTGGTTTCAGCTATGATTCAGGTAGGCTGCGCTG 1620
Db |||||||
QY 1621 GGCATGACACACAGCCTCTTAGTCTTC 1647
Db |||||||
QY 1621 GGCATGACACACAGCCTCTTAGTCTTC 1647
Db |||||||

RESULT 2

AA003320
ID AAD03320 standard; cDNA; 2115 BP.

XX

AC AAD03320;

XX

DT 13-JUN-2001 (first entry)

XX

DE Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.

XX

KW Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;

KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;

KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;

KW cystathione beta synthase; CBS; cardiant; gene therapy; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS

FT 1..1395

FT /*tag= a

FT /product= "Human complete Prkag3 protein"

XX

PN WO200120003-A2.

XX

PD 22-MAR-2001.

XX

PF 11-SEP-2000; 2000WO-EP09896.

XX

PR 10-SEP-1999; 99EP-0402236.

XX

PR 18-MAY-2000; 2000EP-0401388.

XX

(INRG) INRA INST NAT RECH AGRONOMIQUE.

PA (ANDE/) ANDERSSON L.

PA (LOOF/) LOOFT C.

PA (KALM/) KALM E.

XX

PI Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;

PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;

XX

DR WPI; 2001-244810/25.

XX

DR P-PSDB; AAE00223.

XX

New variants of the gamma subunit of vertebrate adenosine

PT monophosphate-activated kinase for diagnosis or treatment of disorders

PT associated with energy metabolism such as diabetes, obesity, and

PT myopathy

XX

Claim 12; Page 65-68; 71pp; English.

PS

The present sequence is a cDNA encoding human adenosine monophosphate

CC (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,

CC complete PRKAG3. Mutation in Prkag3 results in an altered regulation of

CC carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is

CC useful as therapeutic for treating carbohydrate metabolism disorders such

CC as diabetes, obesity, and disorders associated with muscle metabolism

CC such as myopathy and cardiovascular diseases, to modulate AMPK

CC activity and for restoring a normal AMPK function. PRKAG3 sequence

CC and its functionally altered mutants are useful for the diagnostic

CC evaluation, genetic testing and prognosis of a metabolic disorder.

CC preferably a carbohydrate metabolism disorder. Primers that can detect

CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are

CC useful for detecting a dysfunction of carbohydrate metabolism resulting

CC from the expression of a functionally altered allele of PRKAG3.

CC Transgenic animal and host cell transformed with PRKAG3 or a

CC

CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
CC screening compounds able to modulate AMPK activity. Nucleic acid
CC encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
CC in a sequence encoding the first cystathione beta synthase (CBS) domain
CC of PRKAG3 and is useful in gene therapy.

XX
SQ Sequence 2115 BP; 460 A; 622 C; 562 G; 471 T; 0 other;

Query Match 83.3%; Score 1372; DB 22; Length 2115;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 95 ATGAGCTTCCTAGAGCAAGAAAACAGCAGCTCATGGCCATCACCAGCTGTGACCAAGCAGC 154

Db |||||||

QY 155 TCAGAAAGAAATCCGTGGGAAACGGAGGCCAAAGCCTTGAGATGGACAAGGACAGAGTTCG 214

Db |||||||

QY 61 TCAGAAAGAAATCCGTGGGAAACGGAGGCCAAAGCCTTGAGATGGACAAGGACAGAGTTCG 120

QY 215 GTGAGGAAAGGGAGGCCACCAAGGTTCAGGGGAAAGGTCCCGGTCCAGGCCAGCTGCTGAG 274

Db |||||||

QY 121 GTGAGGAAAGGGAGGCCACCAAGGTTCAGGGGAAAGGTCCCGGTCCAGGCCAACTGCTGAG 180

QY 275 TCCACCGGGCTGGAGGCCACATTCCTCCAAAGACACACCTTTGGCTCAAGCTGATCTGCC 334

Db |||||||

QY 181 TCCACCGGGCTGGAGGCCACATTCCTCCAAAGACACACCTTTGGCTCAAGCTGATCTGCC 240

QY 335 GGGTGGGCACCTCCACCAAGGGTGGAGCTGCTCCCTCCCTGACTGTACAGCTCAGCT 394

Db |||||||

QY 241 GGGTGGGCACCTCCACCAAGGGTGGAGCTGCTCCCTCCCTGACTGTACAGCTCAGCT 300

QY 395 GCAGGCTCCAGCACAGATGATGTGGAGCTGGCCACGAGGATTCACAGCCACAGAGGCCCTGG 454

Db |||||||

QY 455 GAGTGTGAGCTAGAGGCCCTGCTGGAAGAGAGGCTGCTCCCTGCTGCTGCTCCCGCAGGCC 514

Db |||||||

QY 361 GAGTGTGAGCTAGAGGCCCTGCTGGAAGAGAGGCTGCTCCCTGCTGCTGCTCCCGCAGGCC 420

QY 515 CCATTTCCCAAGCTGGGCTGGGATGACGAACCTCGGAAACCCCGGCCAGATCTACATG 574

Db |||||||

QY 421 CCATTTCCCAAGCTGGGCTGGGATGACGAACCTCGGAAACCCCGGCCAGATCTACATG 480

QY 575 CGTTTATGAGGAGCACACCTCTACGATGCCATGGCAACTAGCTCCAAAGCTAGTCAATC 634

Db |||||||

QY 481 CGCTTCATGAGGAGCACACCTCTACGATGCCATGGCAACTAGCTCCAAAGCTAGTCAATC 540

QY 635 TTCGACACCATGCTGGAGATCAAGAGGCCCTTCTTTGCTCTGCTGGCCAAACGGTGTGCGG 694

Db |||||||

QY 541 TTCGACACCATGCTGGAGATCAAGAGGCCCTTCTTTGCTCTGCTGGCCAAACGGTGTGCGG 600

QY 695 GCAGCCCTCTATGGGACACAAAGAGCAGAGCTTTGTGGGATGCTGACCATCACTGAC 754

Db |||||||

QY 601 GCAGCCCTCTATGGGACACAAAGAGCAGAGCTTTGTGGGATGCTGACCATCACTGAC 660

QY 755 TTCATCTGCTGCTGATCGCTACTACAGTCCCTCCCTGCTCCAGATCTATGAGATTGAA 814

Db |||||||

QY 661 TTCATCTGCTGCTGATCGCTACTACAGTCCCTCCCTGCTCCAGATCTATGAGATTGAA 720

QY 815 CAACATAAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCTCTGGTC 874

Db |||||||

QY 721 CAACATAAGATTGAGACCTGGAGGAGATCTACCTGCAAGGCTGCTTCAAGCTCTGGTC 780

QY 875 TCCATCTCTCTAATGATAGCCTGTTTGAAGCTGTCTACACCTCTATCAAGAACCGGATC 934

Db |||||||

QY 781 TCCATCTCTCTAATGATAGCCTGTTTGAAGCTGTCTACACCTCTATCAAGAACCGGATC 840

QY 935 CATGGCTGCTGCTGTTTCTGACCCGGTGTGAGGCAAGTACTCCACATCTCTACACAAA 994

Db |||||||

QY 841 CATGGCTGCTGCTGTTTCTGACCCGGTGTGAGGCAAGTACTCCACATCTCTACACAAA 900

QY 995 CGCTCTCTCAAGTTCCTGACATCTTTGTTCTCTGCTGCTCCCGGCCCTCTCTCTAC 1054

Db 901 CGCCTGCTCAAGTCTCTGCACATCTTTGGTTCCCTGCTGCCCGCCCTCTCTCTCTAC 960
Oy 1055 CGCACTATCCAGATTGTTGGGATCGGCATATCCAGACTTGGCTGTGGTCTGGAGACA 1114
Db 961 CGCACTATCCAGATTGTTGGGATCGGCATATCCAGACTTGGCTGTGGTCTGGAGACA 1020
Oy 1115 GCACCCATCTGACTGCACTGGACATCTTTGTGGACCGCGTGTGTCTGCACTCCCTGTG 1174
Db 1021 GCACCCATCTGACTGCACTGGACATCTTTGTGGACCGCGTGTGTCTGCACTCCCTGTG 1080
Oy 1175 GTCAACGAATGTGTCAGTCTGGGCTCTATTCCCGCTTTGATGTGATTCACCTGGCT 1234
Db 1081 GTCAACGAATGTGTCAGTCTGGGCTCTATTCCCGCTTTGATGTGATTCACCTGGCT 1140
Oy 1235 GCCCAGCAACCTCAACCCCTCGACATGATGTGGGAGAGCCCTGAGGCAGAGGACA 1294
Db 1141 GCCCAGCAACCTCAACCCCTCGACATGATGTGGGAGAGCCCTGAGGCAGAGGACA 1200
Oy 1295 CTATGCTGGAGGAGTCTTTCTGTCAGCCGCCACGAGACTTGGGGAGTGTATCGAC 1354
Db 1201 CTATGCTGGAGGAGTCTTTCTGTCAGCCGCCACGAGACTTGGGGAGTGTATCGAC 1260
Oy 1355 AGGATTCTCGGAGCAGGTACACAGCTGTGTCTAGTGGACGAGACCCAGCATCTCTTG 1414
Db 1261 AGGATTCTCGGAGCAGGTACACAGCTGTGTCTAGTGGACGAGACCCAGCATCTCTTG 1320
Oy 1415 GGCCTGCTCTCCCTCTCCGACATCTTTGAGCACTGTGTCTGAGCTCTCAATCCCAAGCCA 1517
Db 1321 GGCCTGCTCTCCCTCTCCGACATCTTTGAGCACTGTGTCTGAGCTCTCAATCCCAAGCCA 1423
Oy 1475 GCCCTCGGGGCTGAGAGATCTGAGTCTCTCAATCCCAAGCCA 1517
Db 1381 GCCCTCGGGGCTGAGAGATCTGAGTCTCTCAATCCCAAGCCA 1423

RESULT 3

AAD03296
ID AAD03296 standard; DNA; 2109 BP.

XX AAD03296;
AC
XX
XX
DT 13-JUN-2001 (first entry)
XX
DE Human AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
XX
KW Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
KW cystathione beta synthase; CBS; cardiant; gene therapy; ss.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH 5'UTR 1..471
FT /*tag= a
FT CDS 472..1389
FT /*tag= b
FT FT /product= "Human Prkag3 protein"
FT 3'UTR 1390..2109
FT /*tag= c
XX
PN W0200120003-A2.
XX
PD 22-MAR-2001.
XX
PF 11-SEP-2000; 2000WO-EP09896.
XX
PR 10-SEP-1999; 99EP-0402236.
PR 18-MAY-2000; 2000EP-0401388.
XX
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
PA (ANDE/) ANDERSSON L.

(LOOF/) LOOFT C.
(KALM/) KALM E.
Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
Tannuccelli N, Gellin J, Le Roy P, Chardon P;
XX
XX WPI; 2001-244810/25.
DR P-PSDB; AAE00221.
XX
XX New variants of the gamma subunit of vertebrate adenosine
PT monophosphate-activated kinase for diagnosis or treatment
PT associated with energy metabolism such as diabetes, obesity, and
PT myopathy -
XX
XX Claim 12; Fig 2; 71pp; English.
XX
XX The present sequence is a cDNA encoding human adenosine monophosphate
CC (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,
CC PRKAG3. Mutation in Prkag3 results in an altered regulation of
CC carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is
CC useful as therapeutic for treating carbohydrate metabolism disorders such
CC as diabetes, obesity, and disorders associated with muscle metabolism
CC such as myopathy and cardiovascular diseases, to modulate AMPK
CC activity, and for restoring a normal AMPK function. PRKAG3 sequence
CC and its functionally altered mutants are useful for the diagnostic
CC evaluation, genetic testing and prognosis of a metabolic disorder,
CC preferably a carbohydrate metabolism disorder. Primers that can detect
CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
CC useful for detecting a dysfunction of carbohydrate metabolism resulting
CC from the expression of a functionally altered allele of PRKAG3.
CC Transgenic animal and host cell transformed with PRKAG3 or a
CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
CC screening compounds able to modulate AMPK activity. Nucleic acid
CC encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
CC in a sequence encoding the first cystathione beta synthase (CBS) domain
CC of PRKAG3 and is useful in gene therapy.
XX
XX Sequence 2109 BP; 458 A; 621 C; 560 G; 470 T; 0 other;

Query Match 82.9%; Score 1366; DB 22; Length 2109;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1416; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 101 TTCTAGAGCAAGAAACAGCAGCTCATGGCCATCACAGCTGTGACAGAGTCTCAGAA 160
Db 1 TTCTAGAGCAAGAAACAGCAGCTCATGGCCATCACAGCTGTGACAGAGTCTCAGAA 60
Oy 161 AGAATCCGTGGAAACCGAGGGCCAAAGCCTTGAGATGGCAAGGACAGAGTCTCGTGGAG 220
Db 61 AGAATCCGTGGAAACCGAGGGCCAAAGCCTTGAGATGGCAAGGACAGAGTCTCGTGGAG 120
Oy 221 GAAGGGAGCCACAGGTCTAGGGGAAAGGTCCCGGTCCAGGCCAGCTGTGAGTCCACC 280
Db 121 GAAGGGAGCCACAGGTCTAGGGGAAAGGTCCCGGTCCAGGCCAGCTGTGAGTCCACC 180
Oy 281 GGGCTGGAGGCCACATTTCCCAAGACACACCTTGGCTCAAGCTGATCTTCCCGGGGTG 340
Db 181 GGGCTGGAGGCCACATTTCCCAAGACACACCTTGGCTCAAGCTGATCTTCCCGGGGTG 240
Oy 341 GGCATCTCCACCAACAGGGTGGGACTGCTCCCTCTGACTGTACAGCTCTCAGCTGCAGGC 400
Db 241 GGCATCTCCACCAACAGGGTGGGACTGCTCCCTCTGACTGTACAGCTCTCAGCTGCAGGC 300
Oy 401 TCCAGACAGATGATGTGGAGCTGGCCACGAGTTCCAGCCACAGAGGCTGGAGTGT 460
Db 301 TCCAGACAGATGATGTGGAGCTGGCCACGAGTTCCAGCCACAGAGGCTGGAGTGT 360
Oy 461 GAGCTAGAAGCCCTGCTGGAGAGAGGCCCTTGCCTGTGCTGCTCCCGAGGCCCTTTT 520
Db 361 GAGCTAGAAGCCCTGCTGGAGAGAGGCCCTTGCCTGTGCTGCTCCCGAGGCCCTTTT 420
Oy 521 CCAAGCTGGGCTGGGATGACGAATCGGAAACCCCGGCCCCAGATCTCATGCGCTTC 580
XX

Db	421	CCCAAGCTGGCGCTGGGATGACGAACCTGCGGAAACCCGGCGCCAGCATCTACATGCGCTTC	480
Qy	581	ATGCAGGAGCACACCTGCTACGATGCGCATGCGCAACTAGCTCCAAGCTAGTCATCTTCGAC	640
Db	481	ATGCAGGAGCACACCTGCTACGATGCGCATGCGCAACTAGCTCCAAGCTAGTCATCTTCGAC	540
Qy	641	ACCATGCTGGAGATCAAGAAGGCCCTCTTTGCTCTGGTGGCCAAACGGTGTGGGGCAGCC	700
Db	541	ACCATGCTGGAGATCAAGAAGGCCCTCTTTGCTCTGGTGGCCAAACGGTGTGGGGCAGCC	600
Qy	701	CCTCTATGGGACACGAGAAGCAGACTTTGTGGGATGCTGACCATCACTGACTTCATC	760
Db	601	CCTCTATGGGACACGAGAAGCAGACTTTGTGGGATGCTGACCATCACTGACTTCATC	660
Qy	761	CTGTGCTGCATCGCTACTACAGGTCCCCCTGGTCCAGATCTATGAGATTGAACAACAT	820
Db	661	CTGTGCTGCATCGCTACTACAGGTCCCCCTGGTCCAGATCTATGAGATTGAACAACAT	720
Qy	821	AAGATTGAGACCTGGAGGGAGATCTACTGCGAAGGCTGCTTCAAGCCTCTGGTCTCCATC	880
Db	721	AAGATTGAGACCTGGAGGGAGATCTACTGCGAAGGCTGCTTCAAGCCTCTGGTCTCCATC	780
Qy	881	TCTCCTAATGATAGCTGTTTTGAAGCTGTCTACACCCTCATCAAGAACCGGATCCATCGC	940
Db	781	TCTCCTAATGATAGCTGTTTTGAAGCTGTCTACACCCTCATCAAGAACCGGATCCATCGC	840
Qy	941	CTGCTCTTCTTGACCCGGTGTGAGGCAACGACTCCACATCCTCACACAAACGGCGTG	1000
Db	841	CTGCTCTTCTTGACCCGGTGTGAGGCAACGACTCCACATCCTCACACAAACGGCGTG	900
Qy	1001	CTCAAGTTCTTGACACATCTTTTGGTTCCTGTGCTGCCCGGCCCTCCTTCTCTACGGACT	1060
Db	901	CTCAAGTTCTTGACACATCTTTTGGTTCCTGTGCTGCCCGGCCCTCCTTCTCTACGGACT	960
Qy	1061	ATCCAAGATTTGGGCATCGGCACATTCGCGAGACTTGGCTGTGGTGTGGACAGCACC	1120
Db	961	ATCCAAGATTTGGGCATCGGCACATTCGCGAGACTTGGCTGTGGTGTGGACAGCACC	1020
Qy	1121	ATCTGACTGCACCTGGACATCTTTTGGACCGCGCGTGTGCTGCACTGCCTGTGGTCAAC	1180
Db	1021	ATCTGACTGCACCTGGACATCTTTTGGACCGCGCGTGTGCTGCACTGCCTGTGGTCAAC	1080
Qy	1181	GAATGTGGTCAGTGTGGGCTCTATTCCCGCTTTGATGTGATTCACCTGGCTGCCGAG	1240
Db	1081	GAATGTGGTCAGTGTGGGCTCTATTCCCGCTTTGATGTGATTCACCTGGCTGCCGAG	1140
Qy	1241	CAAACTTACAAACACCTGGACATGAGTGTGGAGAACGCCCTGAGGACAGACACATATGT	1300
Db	1141	CAAACTTACAAACACCTGGACATGAGTGTGGAGAACGCCCTGAGGACAGACACATATGT	1200
Qy	1301	CTGAGGGAGTCTCTTCTGCCAGCCCCACGAGACTTGGGGAGTGATCGACAGGATT	1360
Db	1201	CTGAGGGAGTCTCTTCTGCCAGCCCCACGAGACTTGGGGAGTGATCGACAGGATT	1260
Qy	1361	GCTCGGAGCAGGTACACAGGCTGTGCTAGTGTGAGAGAGCCAGCATCTCTTGGGGGTG	1420
Db	1261	GCTCGGAGCAGGTACACAGGCTGTGCTAGTGTGAGAGAGCCAGCATCTCTTGGGGGTG	1320
Qy	1421	GTCTCCCTCTCCGACATCTCTTCAAGGCACTGGTGTCTCAGCCCTGTGGCATCGATGCCCTC	1480
Db	1321	GTCTCCCTCTCCGACATCTCTTCAAGGCACTGGTGTCTCAGCCCTGTGGCATCGATGCCCTC	1380
Qy	1481	GGGGCTTGAGAAGATCTGAGTCTCTCAATCCCCAAGCCA	1517
Db	1381	GGGGCTTGAGAAGATCTGAGTCTCTCAATCCCCAAGCCA	1417

RESULT 4
AAH43682
ID AAH43682 standard; DNA; 989 BP.
XX
AC AAH43682;
XX

DT	21-JAN-2002 (first entry)
XX	
DE	PRKAG3 intron 2 - intron 4.
XX	
KW	Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ds.
KW	
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Location/Qualifiers
FT	1..21
FT	/*tag= a
FT	/number= "Intron 2"
FT	/note= "3' portion of intron 2"
FT	22..177
FT	/*tag= b
FT	/number= "Exon 3"
FT	178..541
FT	/*tag= c
FT	/number= "Intron 3"
FT	542..945
FT	/*tag= d
FT	/number= "Exon 4"
FT	946..989
FT	/*tag= e
FT	/number= "Intron 4"
FT	/note= "5' portion of intron 4"
XX	
PN	W02000177305-A2.
XX	
XX	18-OCT-2001.
PD	
XX	
XX	06-APR-2001; 2001WO-SE00765.
PF	
XX	
XX	07-APR-2000; 2000US-195665P.
PR	
XX	(AREX-) AREXIS AB.
PA	
XX	
PI	Andersson L, Luthman H, Marklund S;
XX	
DR	WPI; 2001-657170/75.
XX	
PT	New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the variant -
PT	
XX	
PS	Example 1; Fig 2; 25pp; English.
XX	
CC	The sequences given in AAH43681-84 represents genomic fragments encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution p11A; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation in intron 6.
CC	
XX	Sequence 989 BP; 229 A; 306 C; 286 G; 168 T; 0 other;
SQ	

	Query Match	24.7%	Score 406;	DB 22;	Length 989;
	Best Local Similarity	100.0%;	Pred. No. 3.5e-185;		
	Matches 406;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps
Qy	247	AGGTCCCGGTCCAGGCCAGCTGCTGAGTCCACCGGCTGGAGGCCACATTTCCCCAAAGC	306		
Db	540	AGGTCCCGGTCCAGGCCAGCTGCTGAGTCCACCGGCTGGAGGCCACATTTCCCCAAAGC	599		
Qy	307	CACACCCCTTGGCTCAAGCTGATCTCTCGGGGTGGGCATCTCCACCAACAGGGTGGCACTG	366		

AAH43684
ID AAH43684 standard; DNA; 1014 BP.
AC AAH43684;
XX
DT 21-JAN-2002 (first entry)
DE PRKAG3 intron 10 - 3'UTR.
XX
KW Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
KW metabolic disease; diabetes; obesity; substitution; ds.
XX
OS Homo sapiens.
XX
FH Key
FT intron
FT Location/Qualifiers
FT 1..41
FT /*tag= a
FT /number= "Intron 10"
FT /note= "3' portion of intron 10"
FT 42..79
FT /*tag= b
FT /number= "Exon 11"
FT 80..249
FT /*tag= c
FT /number= "Intron 11"
FT 250..396
FT /*tag= d
FT /number= "Exon 12"
FT 397..739
FT /*tag= e
FT /number= "Intron 12"
FT 740..856
FT /*tag= f
FT /number= "Exon 13"
FT 857..1014
FT /*tag= g
XX
PN WO200177305-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-SE00765.
XX
PR 07-APR-2000; 2000US-195665P.
XX
PA (AREX-) AREXIS AB.
XX
PI Andersson L, Luthman H, Marklund S;
XX
DR WPI; 2001-657170/75.
XX
PT New variants of human AMP-activated protein kinase gamma3 subunit
PT associated with a metabolic disease e.g. diabetes or obesity and method
PT for determining a risk estimate of diseases in subject by detecting the
PT variant -
XX
PS Example 1; Fig 4; 25pp; English.
XX
CC The sequences given in AAH43681-84 represents genomic fragments
CC encoding the human AMP-activated protein kinase gamma 3 subunit
CC (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant,
CC is useful in determining a risk estimate of a metabolic disease,
CC such as diabetes or obesity, in a subject. The variation may occur
CC in exons 3, 4 or 10. In exon 3 variation may be a substitution of
CC a G for a C at nucleotide 320, resulting in the amino acid
CC substitution P71A; in exon 4 variation may be a substitution of a
CC T for a C at nucleotide 550; and in exon 10 variation may be a
CC substitution of a T for a C at nucleotide 1037, resulting in the
CC amino acid substitution R340W. There may also be nucleotide variation
CC in intron 6.
XX
SQ Sequence 1014 BP; 192 A; 325 C; 271 G; 226 T; 0 other;

Query Match 16.9%; Score 278; DB 22; Length 1014;
Best Local Similarity 100.0%; Pred. No. 1.5e-123;
Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1370 CAGGTACACAGGCTGGTCTAGTGGACGAGACCCAGCATCTCTTGGGGCTGCTCCCTC 1429
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 737 CAGGTACACAGGCTGGTCTAGTGGACGAGACCCAGCATCTCTTGGGGCTGCTCCCTC 796
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1430 TCCGACATCTCTTCCAGGCACTGGTCTCAGCCCTCTGCGCATCGCTCGGGGCTTGA 1489
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 797 TCCGACATCTCTTCCAGGCACTGGTCTCAGCCCTCTGCGCATCGCTCGGGGCTTGA 856
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1490 GAAGATCTGAGTCTCTCAATCCCAAGCCACCTGCACACCTGGAAGGGAACCTG 1549
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 857 GAAGATCTGAGTCTCTCAATCCCAAGCCACCTGCACACCTGGAAGGGAACCTG 916
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1550 GAGAACTCAGCCTTTCATCTTCCCCCCCCCATTTGCTGGTTCAGCTATGATTCAGGTAG 1609
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 917 GAGAACTCAGCCTTTCATCTTCCCCCCCCCATTTGCTGGTTCAGCTATGATTCAGGTAG 976
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1610 GCTCTGCCCTGGGCCATGACACACGACCTCTTAGTCTTTC 1647
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 977 GCTCTGCCCTGGGCCATGACACACGACCTCTTAGTCTTTC 1014
RESULT 7
AAK72740/c
ID AAK72740 standard; DNA; 3425 BP.
XX
AC AAK72740;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27552.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.


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FT XX /note= "5' portion of intron 10"
PN XX
XX WO200177305-A2.
XX
PD 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-SE00765.
XX PF
XX 07-APR-2000; 2000US-195665P.
XX PR
XX (AREX-) AREXIS AB.
XX PA
XX Andersson L, Luthman H, Marklund S;
XX WIPI; 2001-657170/75.
XX DR
XX
XX New variants of human AMP-activated protein kinase gamma3 subunit
PT associated with a metabolic disease e.g. diabetes or obesity and method
PT for determining a risk estimate of diseases in subject by detecting the
PT variant -
XX
XX Example 1; Fig 3; 25pp; English.
PS
XX
XX The sequences given in AAH43681-84 represents genomic fragments
CC encoding the human AMP-activated protein kinase gamma 3 subunit
CC (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant,
CC is useful in determining a risk estimate of a metabolic disease,
CC such as diabetes or obesity, in a subject. The variation may occur
CC in exons 3, 4 or 10. In exon 3 variation may be a substitution of
CC a G for a C at nucleotide 320, resulting in the amino acid
CC substitution P71A; in exon 4 variation may be a substitution of a
CC T for a C at nucleotide 550; and in exon 10 variation may be a
CC substitution of a T for a C at nucleotide 1037, resulting in the
CC amino acid substitution R340W. There may also be nucleotide variation
CC in intron 6.
XX
XX Sequence 1722 BP; 321 A; 504 C; 534 G; 363 T; 0 other;
SQ
Query Match 10.2%; Score 168; DB 22; Length 1722;
Best Local Similarity 100.0%; Pred. No. 1.5e-70;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1022 GGTTCCTGCTGCGCCGCTCTTCTTACCGCACTATCCAGATTTGGGCATCGGC 1081
DB 1523 GGTTCCTGCTGCGCCGCTCTTCTTACCGCACTATCCAGATTTGGGCATCGGC 1502
QY 1082 ACATTCCGAGACTTGGCTGTGGTCTGGAGACAGCACCCATCCTGACTGCATCGACATC 1141
DB 1583 ACATTCCGAGACTTGGCTGTGGTCTGGAGACAGCACCCATCCTGACTGCATCGACATC 1642
QY 1142 TTTGTGACCGCGCTGTGTCTGCACTGCCTGTGGTCAACGAATGTGGT 1189
DB 1643 TTTGTGACCGCGCTGTGTCTGCACTGCCTGTGGTCAACGAATGTGGT 1690
RESULT 10
ABA44706/c
ID ABA44706 standard; DNA; 378 BP.
XX
XX ABA44706;
AC
XX
DT 01-FEB-2002 (first entry)
XX
DE Human breast cell single exon nucleic acid probe #3401.
XX
XX Human; microarray; single exon probe; gene expression; breast;
KW disease; cancer; es.
XX
XX Homo sapiens.
OS
XX WO200157271-A2.
PN
XX 09-AUG-2001.
PD
```

```
XX 30-JAN-2001; 2001WO-US00662.
PF
XX
XX 04-FEB-2000; 2000US-0180312.
PR
XX 26-MAY-2000; 2000US-0207456.
PR
XX 30-JUN-2000; 2000US-0608408.
PR
XX 03-AUG-2000; 2000US-0632366.
PR
XX 21-SEP-2000; 2000US-0234687.
PR
XX 27-SEP-2000; 2000US-0236359.
PR
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WIPI; 2001-496933/54.
XX
XX New spatially-addressable set of single exon nucleic acid probes,
PT useful for measuring gene expression in sample derived from human
PT breast, comprises number of single exon nucleic acid probes -
XX
XX Claim 1; SEQ ID NO 3401; 327pp + sequence listing; English.
XX
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and Br 474 cells. The method involves contacting
CC the probes with a collection of detectably labelled nucleic acids
CC derived from mRNA of human breast, and then measuring the label
CC bound to each probe of the microarray. The probes are useful for
CC verifying the expression of regions of genomic DNA predicted to
CC encode proteins. They are useful for gene discovery, and for
CC determining predisposition and/or prognosing breast disease. Gene
CC expression analysis is useful for assessing the toxicity of chemical
CC agents on cells. The microarray of this invention presents a far greater
CC diversity of probes for measuring gene expression, with far less bias
CC than expressed sequence tag microarrays. The method is suitable for
CC rapid production of functional information from genomic sequence. The
CC present sequence is a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
SQ
Query Match 5.2%; Score 85; DB 22; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.4e-30;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 651 AGATCAAGAGGCGCTTCTTGTCTGCTGCGCAACGGTGTGCGGCGAGCCCTCTATGGG 710
DB 351 AGATCAAGAGGCGCTTCTTGTCTGCTGCGCAACGGTGTGCGGCGAGCCCTCTATGGG 292
QY 711 ACAGCAAGAGCAGAGCTTTGTGGG 735
DB 291 ACAGCAAGAGCAGAGCTTTGTGGG 267
RESULT 11
ABA55162/c
ID ABA55162 standard; DNA; 378 BP.
XX
XX ABA55162;
AC
XX
DT 01-FEB-2002 (first entry)
XX
XX Human foetal liver single exon nucleic acid probe #3467.
DE
XX Human; foetal liver; gene expression; single exon nucleic acid probe; es.
KW
XX Homo sapiens.
OS
XX WO200157277-A2.
PN
XX
```


XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483446/52.

XX Single exon nucleic acid probes for analyzing gene expression in human

PT brains -

XX

PS Example 4; SEQ ID NO: 3414; 650pp + Sequence Listing; English.

XX

CC The present invention provides a number of single exon nucleic acid

CC probes which are derived from genomic sequences expressed in the human

CC brain. They can be used to measure gene expression in brain cell samples,

CC which may enable the diagnosis and improved treatment of nervous system,

CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,

CC epilepsy and cancers. The present sequence is one of the probes of the

CC invention.

XX

XX Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;

XX

Query Match 5.2%; Score 85; DB 22; Length 378;

Best Local Similarity 100.0%; Pred. No. 1.4e-30;

Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 651 AGATCAAGAAGCCCTCTTTGCTCTGGTGGCCAAACGGTGTGGGGCAGCCCTCTATGGG 710

Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

351 AGATCAAGAAGCCCTCTTTGCTCTGGTGGCCAAACGGTGTGGGGCAGCCCTCTATGGG 292

Oy 711 ACAGCAAGAAGCAGAGCTTTGTGGG 735

Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

291 ACAGCAAGAAGCAGAGCTTTGTGGG 267

RESULT 14

AAK28874/c

ID AAK28874 standard; DNA; 378 BP.

XX

AC AAK28874;

XX

XX 06-NOV-2001 (first entry)

XX Human bone marrow expressed single exon probe SEQ ID NO: 3431.

XX

DE Human; bone marrow expressed exon; gene expression analysis; probe;

XX microarray; cancer; leukaemia; lymphoma; myeloma; ss.

XX

OS Homo sapiens.

XX

XX WO200157276-A2.

XX

XX 09-AUG-2001.

XX

XX 30-JAN-2001; 2001WO-US00668.

XX

XX 04-FEB-2000; 2000US-0180312.

XX

XX 26-MAY-2000; 2000US-0207456.

XX

XX 30-JUN-2000; 2000US-0608408.

XX

XX 03-AUG-2000; 2000US-0632366.

XX

XX 21-SEP-2000; 2000US-0234687.

XX

XX 27-SEP-2000; 2000US-0236359.

XX

XX 04-OCT-2000; 2000GB-0024263.

XX

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX

XX WPI; 2001-488900/53.

XX

XX Human genome-derived single exon nucleic acid probes useful for

PT analyzing gene expression in human bone marrow -

XX

PS Example 4; SEQ ID NO: 3431; 658pp + Sequence Listing; English.

XX

CC The present invention provides a number of single exon nucleic acid

CC probes which are derived from genomic sequences expressed in the human

CC bone marrow. They can be used to measure gene expression in bone marrow

CC samples, which may enable the improved diagnosis and treatment of cancers

CC such as lymphoma, leukaemia and myeloma. The present sequence is one of

CC the probes of the invention.

XX

XX Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;

XX

Query Match 5.2%; Score 85; DB 22; Length 378;

Best Local Similarity 100.0%; Pred. No. 1.4e-30;

Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 651 AGATCAAGAAGCCCTCTTTGCTCTGGTGGCCAAACGGTGTGGGGCAGCCCTCTATGGG 710

Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

351 AGATCAAGAAGCCCTCTTTGCTCTGGTGGCCAAACGGTGTGGGGCAGCCCTCTATGGG 292

Oy 711 ACAGCAAGAAGCAGAGCTTTGTGGG 735

Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

291 ACAGCAAGAAGCAGAGCTTTGTGGG 267

RESULT 15

AAI13465/c

ID AAI13465 standard; DNA; 378 BP.

XX

AC AAI13465;

XX

XX 12-OCT-2001 (first entry)

XX

DE Probe #3398 for gene expression analysis in human cervical cell sample.

XX

XX Probe; human; microarray; gene expression; cervical epithelial cell;

XX cervical cancer; ss.

XX

XX Homo sapiens.

XX

XX WO200157278-A2.

XX

XX 09-AUG-2001.

XX

XX 30-JAN-2001; 2001WO-US00670.

XX

XX 04-FEB-2000; 2000US-0180312.

XX

XX 26-MAY-2000; 2000US-0207456.

XX

XX 30-JUN-2000; 2000US-0608408.

XX

XX 03-AUG-2000; 2000US-0632366.

XX

XX 21-SEP-2000; 2000US-0234687.

XX

XX 27-SEP-2000; 2000US-0236359.

XX

XX 04-OCT-2000; 2000GB-0024263.

XX

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX

XX WPI; 2001-488901/53.

XX

XX Human genome-derived single exon nucleic acid probes useful for

PT analyzing gene expression in human cervical epithelial cells -

XX

XX Claim 25; SEQ ID No 3398; 487pp; English.

XX

XX The present invention relates to human single exon nucleic acid probes

CC (SENP). The present sequence is one such probe. The SENPs are derived

CC from human HeLa cells. The SENPs can be used to produce a single exon

CC microarray, which can be used for measuring human gene expression in a

CC sample derived from human cervical epithelial cells. By measuring gene

CC expression, the probes are therefore useful in grading and/or staging

CC of diseases of the cervix, notably cervical cancer.

CC

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

```
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;

Query Match      5.2%; Score 85; DB 22; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.4e-30;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 651 AGATCAAGAGGCCTTCTTTGCTCTGGTGGCCAAACGGTGTGGGGCAGCCCTCTATGGG 710
Db 351 AGATCAAGAGGCCTTCTTTGCTCTGGTGGCCAAACGGTGTGGGGCAGCCCTCTATGGG 292

Qy 711 ACAGCAAGAGCAGAGCTTTGTGGG 735
Db 291 ACAGCAAGAGCAGAGCTTTGTGGG 267
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OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 09:44:42 ; Search time 2107.51 Seconds
(without alignments)
12656.598 Million cell updates/sec

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Perfect score: 1647
Sequence: 1 ttggtctgggctggccaca.....acaccagcctcttagttcttc 1647

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 15

Total number of hits satisfying chosen parameters: 44986

Minimum DB seq length: 0
Maximum DB seq length: 200000000

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- 2: em_esthum:*
- 3: em_estlin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hic:*
- 9: gb_esti:*
- 10: gb_estc:*
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- 15: em_estfun:*
- 16: em_estcom:*
- 17: gb_gss:*
- 18: em_gss_hum:*
- 19: em_gss_inv:*
- 20: em_gss_pln:*
- 21: em_gss_vrt:*
- 22: em_gss_fun:*
- 23: em_gss_man:*
- 24: em_gss_mus:*
- 25: em_gss_other:*
- 26: em_gss_pro:*
- 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	164	10.0	413	9	AA178898 zp38d10.r
2	68	4.1	485	14	W94830 zai3ei0.r
3	42	2.6	572	13	B1344527 373008 MA
4	41	2.5	399	10	AW356079 38073 MAR
5	41	2.5	422	10	AW427435 63185 MAR
6	41	2.5	444	12	BF990374 291826 MA

7	41	2.5	548	13	B1775360
8	37	2.2	298	10	AW314499
9	24	1.5	461	10	BE126712
10	24	1.5	595	13	BM487789
11	24	1.5	636	12	BG713637
12	24	1.5	687	9	AJ451523
13	24	1.5	758	9	AJ396118
14	23	1.4	474	12	BF601364
15	22	1.3	124	13	B1012981
16	22	1.3	372	13	BM490188
17	22	1.3	563	13	BI555697
18	21	1.3	286	10	BB527609
19	21	1.3	356	10	AW124415
20	21	1.3	356	12	BF456027
21	21	1.3	357	13	BI134322
22	21	1.3	504	12	BF710369
23	21	1.3	518	12	BF999510
24	21	1.3	538	17	AQ431286
25	21	1.3	609	10	BB634609
26	21	1.3	621	10	BB628877
27	21	1.3	655	10	BB629521
28	21	1.3	685	10	BB630381
29	21	1.3	686	17	BH460875
30	21	1.3	697	17	AZ942448
31	21	1.3	933	13	BI662109
32	21	1.3	954	17	AZ690459
33	20	1.2	132	13	BI013023
34	20	1.2	157	10	AV321038
35	20	1.2	222	13	BG997440
36	20	1.2	291	17	AZ745562
37	20	1.2	500	9	AL780430
38	20	1.2	533	9	AI477537
39	20	1.2	548	17	AQ693634
40	20	1.2	549	9	AA562894
41	20	1.2	589	13	BI766104
42	20	1.2	621	9	AA167839
43	20	1.2	660	17	AZ360277
44	20	1.2	789	13	BI871153
45	20	1.2	851	9	AL519471

ALIGNMENTS

RESULT 1
AA178898
LOCUS
DEFINITION
zp38d10.r1 Stratagene muscle 937209 Homo sapiens cDNA clone
IMAGE:611731 5' similar to SW:AAKG_RAT P80385 5'-AMP-ACTIVATED
PROTEIN KINASE, GAMMA CHAIN ;, mRNA sequence.
ACCESSION
AA178898
VERSION
AA178898.1 GI:1760259
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 413)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
TITLE
JOURNAL
COMMENT
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1280 Std Error: 0.00

AA178898 413 bp mRNA linear EST 09-MAR-1998
zp38d10.r1 Stratagene muscle 937209 Homo sapiens cDNA clone
IMAGE:611731 5' similar to SW:AAKG_RAT P80385 5'-AMP-ACTIVATED
PROTEIN KINASE, GAMMA CHAIN ;, mRNA sequence.

Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."

BASE COUNT 106 a 190 c 151 g 124 t 1 others

ORIGIN

Query Match 2.6%; Score 42; DB 13; Length 572;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1247 TACACACCTGGACATGAGTGTGGGAGAGCCCTGAGGCAG 1288
|||||
Db 409 TACAACACCTGGACATGAGTGTGGGAGAGCCCTGAGGCAG 450
|||||

RESULT 4
AW356079

LOCUS
DEFINITION 38073 MARC 2BOV Bos taurus cDNA 5', mRNA linear EST 25-APR-2001
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM Bos taurus

REFERENCE
AUTHORS Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.M., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

JOURNAL
MEDLINE
COMMENT Genome Res. 11 (4), 626-630 (2001)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options.

PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTTCCCGTCCAGCAGC
Plate: 17 row: P column: 9
Seq primer: ATTTAGGTGACACTATAG.

FEATURES
source
1..399
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."
100 a 126 c 117 g 56 t

BASE COUNT 100 a 126 c 117 g 56 t

ORIGIN

Query Match 2.5%; Score 41; DB 10; Length 399;
Best Local Similarity 100.0%; Pred. No. 6.3e-08;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 CAGCTGCTGAGTCCACCGGGCTGGAGGCCACATTTCCCAAG 304
|||||
Db 206 CAGCTGCTGAGTCCACCGGGCTGGAGGCCACATTTCCCAAG 246
|||||

RESULT 5
AW427435

LOCUS
DEFINITION 63185 MARC 3BOV Bos taurus cDNA 5', mRNA linear EST 25-APR-2001
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM Bos taurus

REFERENCE
AUTHORS Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.M., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

JOURNAL
MEDLINE
COMMENT Genome Res. 11 (4), 626-630 (2001)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options.

PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTTCCCGTCCAGCAGC
Plate: 32 row: F column: 22
Seq primer: ATTTAGGTGACACTATAG.

FEATURES
source
1..422
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinosus muscle, and fetal longissimus muscle."
102 a 136 c 125 g 59 t

BASE COUNT 102 a 136 c 125 g 59 t

ORIGIN

Query Match 2.5%; Score 41; DB 10; Length 422;
Best Local Similarity 100.0%; Pred. No. 6.4e-08;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 CAGCTGCTGAGTCCACCGGGCTGGAGGCCACATTTCCCAAG 304
|||||
Db 254 CAGCTGCTGAGTCCACCGGGCTGGAGGCCACATTTCCCAAG 294
|||||

RESULT 6
BF890374

LOCUS
DEFINITION 291826 MARC 3BOV Bos taurus cDNA 5', mRNA linear EST 25-APR-2001
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM Bos taurus

REFERENCE
AUTHORS Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,

Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W., Rohrer, G.A., Chitko-McKown, C.G., Perteau, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

Genome Res. 11 (4), 626-630 (2001)

21180013

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTTCCAGTCACGACG

Plate: 57 row: H column: 11

Seq primer: ATTTAGGTGACACTATAG.

Location/Qualifiers

1..444

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone_lib="MARC 3BOV"

/tissue_type="pooled"

/lab_host="DH108"

/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinosus muscle, and fetal longissimus muscle."

BASE COUNT 91 a 147 c 139 g 67 t

ORIGIN

Query Match

Best Local Similarity 2.5%; Score 41; DB 12; Length 444;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 264 CAGCTGCTGAGTCCACCGGGCTGGAGGCCACATTTCCCAAG 304

Db 59 CAGCTGCTGAGTCCACCGGGCTGGAGGCCACATTTCCCAAG 99

RESULT 7

B1775360

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 548)

Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W., Rohrer, G.A., Chitko-McKown, C.G., Perteau, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

Genome Res. 11 (4), 626-630 (2001)

21180013

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

FEATURES

source

1..548

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone_lib="MARC 3BOV"

/tissue_type="pooled"

Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTTCCAGTCACGACG

Plate: 90 row: I column: 16

Seq primer: ATTTAGGTGACACTATAG.

Location/Qualifiers

1..548

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone_lib="MARC 2BOV"

/tissue_type="pooled"

/lab_host="DH108"

/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

BASE COUNT 119 a 173 c 163 g 93 t

ORIGIN

Query Match

Best Local Similarity 2.5%; Score 41; DB 13; Length 548;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 264 CAGCTGCTGAGTCCACCGGGCTGGAGGCCACATTTCCCAAG 304

Db 101 CAGCTGCTGAGTCCACCGGGCTGGAGGCCACATTTCCCAAG 141

RESULT 8

AW314499

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 298)

Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Perteau, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

Genome Res. 11 (4), 626-630 (2001)

21180013

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTTCCAGTCACGACG

Plate: 11 row: H column: 23

Seq primer: ATTTAGGTGACACTATAG.

Location/Qualifiers

1..298

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone_lib="MARC 3BOV"

/tissue_type="pooled"

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/lab_host="DH108"
/note="Vector: pCMV SPORT6; Site.1: NotI; Site.2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."
BASE COUNT      55 a      96 c      81 g      66 t
ORIGIN

Query Match      2.2%; Score 37; DB 10; Length 298;
Best Local Similarity 100.0%; Pred. No. 4.2e-06;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1298 TGTCTGGAGGAGTCTTTCTCTGCCAGCCACACGAGA 1334
|||||
Db 227 TGTCTGGAGGAGTCTTTCTCTGCCAGCCACGAGA 263
|||||

RESULT 9
BE126712
LOCUS
DEFINITION
DEPA0460 Rat Lambda ZAP Express Library Rattus norvegicus cDNA 5',
mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
AUTHORS
Sleeman, M.A., Murison, J.G., Strachan, L., Kumble, K.D., Glenn, M.P.,
McGrath, A., Grierson, A., Havukkala, I., Tan, P.L.J., and Watson, J.D.
Expressed sequence tags of cDNA clones from rat dermal papilla
cells
JOURNAL
COMMENT
Unpublished (2000)
Contact: Sleeman MA
Biology
Genesis Research and Development Corporation Limited
P.O. Box 50, 1 Fox St, Parnell, Auckland, New Zealand
Tel: 0064 9 373 5600
Fax: 0064 9 373 2189
Email: m.sleeman@genesis.co.nz
Seq primer: T3 forward
High quality sequence stop: 461.
FEATURES
source
Location/Qualifiers
1..461
/organism="Rattus norvegicus"
/strain="Dark-Agouti"
/db_xref="taxon:10116"
/clone_lib="Rat Lambda ZAP Express Library"
/tissue_type="vibrissae"
/cell_type="dermal papilla"
BASE COUNT      117 a      114 c      109 g      121 t
ORIGIN

Query Match      1.5%; Score 24; DB 10; Length 461;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 737 ATGCTGACCATCACTGACTTCATC 760
|||||
Db 246 ATGCTGACCATCACTGACTTCATC 269
|||||

RESULT 10
BM487789
LOCUS
DEFINITION
pgm2n.pk005.j24 Normalized Chicken Breast Muscle, Leg Muscle, and
Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA
clone pgm2n.pk005.j24 5', similar to gb|AAC52580.1 (U42413)
5'-AMP-activated protein kinase, gamma-1 subunit [Rattus norvegicus
], mRNA sequence.
BASE COUNT      55 a      96 c      81 g      66 t
ORIGIN

/lab_host="DH108"
/note="Vector: pCMV SPORT6; Site.1: NotI; Site.2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."
BASE COUNT      55 a      96 c      81 g      66 t
ORIGIN

Query Match      2.2%; Score 37; DB 10; Length 298;
Best Local Similarity 100.0%; Pred. No. 4.2e-06;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1298 TGTCTGGAGGAGTCTTTCTCTGCCAGCCACACGAGA 1334
|||||
Db 227 TGTCTGGAGGAGTCTTTCTCTGCCAGCCACGAGA 263
|||||

RESULT 9
BE126712
LOCUS
DEFINITION
DEPA0460 Rat Lambda ZAP Express Library Rattus norvegicus cDNA 5',
mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
AUTHORS
Sleeman, M.A., Murison, J.G., Strachan, L., Kumble, K.D., Glenn, M.P.,
McGrath, A., Grierson, A., Havukkala, I., Tan, P.L.J., and Watson, J.D.
Expressed sequence tags of cDNA clones from rat dermal papilla
cells
JOURNAL
COMMENT
Unpublished (2000)
Contact: Sleeman MA
Biology
Genesis Research and Development Corporation Limited
P.O. Box 50, 1 Fox St, Parnell, Auckland, New Zealand
Tel: 0064 9 373 5600
Fax: 0064 9 373 2189
Email: m.sleeman@genesis.co.nz
Seq primer: T3 forward
High quality sequence stop: 461.
FEATURES
source
Location/Qualifiers
1..461
/organism="Rattus norvegicus"
/strain="Dark-Agouti"
/db_xref="taxon:10116"
/clone_lib="Rat Lambda ZAP Express Library"
/tissue_type="vibrissae"
/cell_type="dermal papilla"
BASE COUNT      117 a      114 c      109 g      121 t
ORIGIN

Query Match      1.5%; Score 24; DB 10; Length 461;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 737 ATGCTGACCATCACTGACTTCATC 760
|||||
Db 246 ATGCTGACCATCACTGACTTCATC 269
|||||

RESULT 10
BM487789
LOCUS
DEFINITION
pgm2n.pk005.j24 Normalized Chicken Breast Muscle, Leg Muscle, and
Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA
clone pgm2n.pk005.j24 5', similar to gb|AAC52580.1 (U42413)
5'-AMP-activated protein kinase, gamma-1 subunit [Rattus norvegicus
], mRNA sequence.
```

```
BM487789
BM487789.1 GI:18608720
EST.
Chicken.
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 595)
Cogburn, L.A. and Monsonogo-Ornan, E.
ESTs from Normalized Chicken Breast Muscle, Leg Muscle, and
Epiphyseal Growth Plate cDNA library, USDA/IFAPs Animal Genome
Project
Unpublished (2002)
Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest.udel.edu.
FEATURES
source
Location/Qualifiers
1..595
/organism="Gallus gallus"
/strain="Commercial broiler and Ottawa Res. Centre
Strains 90 & 21"
/db_xref="taxon:9031"
/clone="pgm2n.pk005.j24"
/clone_lib="Normalized Chicken Breast Muscle, Leg Muscle,
and Epiphyseal Growth Plate cDNA library (pgm2n)"
/sex="Male and Female"
/tissue_type="Breast muscle, leg muscle and epiphyseal
growth plate"
/dev_stage="Breast, leg; Embryo(d19); post-hatch(1d,1.3,5,7,9
,11 weeks)"
/lab_host="E. coli EMPDH108"
/note="Vector: pCMVSPORT6; Library made from equivalent
pools of total RNA isolated from each tissue (embryonic
muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth
plate 33.3% of the final RNA pool). Single pass sequencing
from 5'-end"
BASE COUNT      126 a      199 c      137 g      133 t
ORIGIN

Query Match      1.5%; Score 24; DB 13; Length 595;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 737 ATGCTGACCATCACTGACTTCATC 760
|||||
Db 146 ATGCTGACCATCACTGACTTCATC 169
|||||

RESULT 11
BG713637
LOCUS
DEFINITION
pglin.pk008.c13 Normalized Liver Library Gallus gallus cDNA clone
pglin.pk008.c13 5', similar to gi|4506061 ref|NP_002724.1| protein
kinase, AMP-activated, gamma 1 non-catalytic subunit; AMPK gamma 1;
protein kinase, AMP-activated, noncatalytic, gamma-1 (Homo sapiens)
gi|12737489 ref|XP_006778.2| protein kinase, AMP-activated, gamma 1
non, mRNA sequence.
BG713637
BG713637.1 GI:14007587
EST.
Chicken.
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 636)
Burnside, J., Morgan, R.W. and Cogburn, L.A.
Chicken ESTs from a normalized liver library
Unpublished (2001)
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
```

```

COMMENT      Contact: Joan Burnside
              Molecular Endocrinology
              University of Delaware
              40 Townsend Hall, Newark, DE 19717, USA
              Tel: 302 831-1345
              Fax: 302-831-3411
              Email: joan@udel.edu, www.chickest.udel.edu.

FEATURES
source
1. 636
/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="pglin.pk008.c13"
/sex="Male and Female"
/tissue_type="liver"
/lab_host="E.coli EMDH10B"
/note="Vector: pCMVSPORT 6"

BASE COUNT  129 a 215 c 167 g 119 t 6 others
ORIGIN

Query Match      1.5%; Score 24; DB 12; Length 636;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 737 ATGCTGACCATCACTGACTTCATC 760
|||||
Db 286 ATGCTGACCATCACTGACTTCATC 309

RESULT 12
AJ451523
LOCUS      687 bp mRNA linear EST 22-APR-2002
DEFINITION riken1 Gallus gallus cDNA clone 29a6r1, mRNA sequence.
ACCESSION AJ451523
VERSION AJ451523.1 GI:20261619
KEYWORDS EST.
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 687)
/tissue_type="bursal lymphocyte EST"
/dev_stage="2-3 weeks old"
/note="CB inbred strain"

REFERENCE
AUTHORS Buerstedde, J.M.
TITLE Gallus gallus bursal lymphocyte EST
JOURNAL Unpublished (2002)
COMMENT Contact: Buerstedde JM
Heinrich-Pette-Institute
Cellular Immunology
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.

FEATURES
source
1. 687
/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="29a6r1"
/clone_lib="riken1"
/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
/note="CB inbred strain"

BASE COUNT  143 a 228 c 191 g 125 t
ORIGIN

Query Match      1.5%; Score 24; DB 9; Length 687;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 737 ATGCTGACCATCACTGACTTCATC 760
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Db 305 ATGCTGACCATCACTGACTTCATC 328

RESULT 13
AJ396118
LOCUS      758 bp mRNA linear EST 25-JAN-2001
DEFINITION dkfz426 Gallus gallus cDNA clone 25f16r1, mRNA sequence.
ACCESSION AJ396118
VERSION AJ396118.1 GI:7127728
KEYWORDS EST.
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 758)
/tissue_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
/note="CB inbred strain"

REFERENCE
AUTHORS J. Korn, B. and Buerstedde, J.M.
TITLE A large database of chicken bursal ESTs as a resource for the
analysis of vertebrate gene function
JOURNAL Genome Res. 10 (12), 2062-2069 (2000)
MEDLINE 20568495
COMMENT Contact: Buerstedde JM
Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.

FEATURES
source
1. 758
/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="25f16r1"
/clone_lib="dkfz426"
/tissue_type="Bursa of Fabricius"
/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"

BASE COUNT  168 a 238 c 186 g 166 t
ORIGIN

Query Match      1.5%; Score 24; DB 9; Length 758;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 737 ATGCTGACCATCACTGACTTCATC 760
|||||
Db 124 ATGCTGACCATCACTGACTTCATC 147

RESULT 14
BF601364
LOCUS      474 bp mRNA linear EST 25-APR-2001
DEFINITION 266320 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BF601364
VERSION BF601364.1 GI:11698586
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 474)
/tissue_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
/note="CB inbred strain"

REFERENCE
AUTHORS Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett
, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Perteau, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
Keele, J.W.
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
JOURNAL Genome Res. 11 (4), 626-630 (2001)
MEDLINE 21180013
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68913-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred

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v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCAGGACG
Plate: 40 row: O column: 13
Seq primer: ATTTAGGTGACACTATAG.

FEATURES

Location/Qualifiers
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/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."
81 a 173 c 119 g 101 t

BASE COUNT

ORIGIN

Query Match 1.4%; Score 23; DB 12; Length 474;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1451 GTGCTCAGCCCTGTCGCATCGA 1473

Db 118 GTGCTCAGCCCTGTCGCATCGA 140

RESULT 15

BI012981/c
LOCUS BI012981 124 bp mRNA linear EST 13-JUN-2001
DEFINITION PM2-ET0206-160101-001-f08 ET0206 Homo sapiens cDNA, mRNA sequence.
ACCESSION BI012981
VERSION BI012981.1 GI:14417052
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE

AUTHORS
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL

MEDLINE

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&t2=PM2-ET0206-
160101-001-f08&t3=2001-01-16&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 16

High quality sequence stop: 124.

FEATURES

source

1. .124
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ET0206"
/dev_stage="Adult"

/note="Organ: lung tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 30 a 26 c 43 g 25 t
ORIGIN

Query Match 1.3%; Score 22; DB 13; Length 124;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1422 TCTCCCTCTCCGACATCCTTCA 1443

Db 107 TCTCCCTCTCCGACATCCTTCA 86

Search completed: January 6, 2003, 11:08:01
Job time : 2115.51 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 09:44:41 ; Search time 329.168 Seconds
(without alignments)
11781.028 Million cell updates/sec

Title: US-09-826-581-3

Perfect score: 1722

Sequence: 1 cctggccctcagatcaaga.....gatgagagctcggctgga 1722

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 15

Total number of hits satisfying chosen parameters: 7349

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_101002.*

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22: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1722	100.0	1722	22	AAH43683
2	346	20.1	378	22	ABA44706
3	346	20.1	378	22	ABA55162
4	346	20.1	378	22	ABA24907
5	346	20.1	378	22	AAK03423
6	346	20.1	378	22	AAK28874
7	346	20.1	378	22	AAI13465
8	346	20.1	378	22	AAI34821
9	346	20.1	378	22	AAI03344

C	10	346	20.1	378	24	ABS03407	Human genome-deriv
	11	168	9.8	1647	22	AAH43685	PRKAG3 cDNA. Homo
	12	168	9.8	2109	22	AAH03296	Human AMPK gamma 8
	13	168	9.8	2115	22	AAH03320	Human AMPK gamma 8
	14	147	8.5	547	22	ABA08485	Human AMP-activate
	15	65	3.8	92	22	ABA49850	Human breast cell
	16	65	3.8	92	22	ABA67769	Human foetal liver
	17	65	3.8	92	22	ABA4826	Probe #13292 for g
	18	65	3.8	92	22	AAK16181	Human brain expres
	19	65	3.8	92	22	AAK41922	Human bone marrow
	20	65	3.8	92	22	AAI22692	Probe #12625 for g
	21	65	3.8	92	22	AAI47988	Probe #16674 used
	22	65	3.8	92	22	AAI08354	Probe #8345 used t
	23	65	3.8	92	22	ABS15953	Human genome-deriv
	24	38	2.2	1867	22	AAH03295	Pig AMPK gamma sub
	25	38	2.2	1873	22	AAH03319	Pig AMPK gamma sub
	26	38	2.2	1873	24	AAH36456	Pig wild-type PRKA
	27	38	2.2	1873	24	AAH36457	Pig PRKAG3 polymor
	28	38	2.2	1873	24	AAH36458	Pig PRKAG3 polymor
	29	38	2.2	1873	24	AAH36459	Pig PRKAG3 polymor
	30	38	2.2	1873	24	AAH36460	Pig PRKAG3 polymor
	31	38	2.2	2022	22	AAH03321	Sus scrofa PRKAG3
	32	24	1.4	5946	13	AAQ28398	Rat nestin gene.
	33	24	1.4	11236	15	AAQ70447	Rat nestin gene.
	34	23	1.3	23	22	AAH43695	PRKAG3 reverse pri
	35	21	1.2	234	24	ABN18013	Human ORFX polynuc
	36	21	1.2	525	22	AAH10581	Human cDNA clone (
	37	19	1.1	23	24	AAH36468	Pig PRKAG3 gene co
	38	19	1.1	190	22	ABA69740	Human foetal liver
	39	19	1.1	190	22	AAK17931	Human brain expres
	40	19	1.1	190	22	AAK43806	Human bone marrow
	41	19	1.1	190	22	AAI49825	Probe #18511 used
	42	19	1.1	190	24	ABS18034	Human genome-deriv
	43	19	1.1	266	21	AAC28698	Human secreted pro
	44	19	1.1	422	21	AAZ65087	Membrane-bound pro
	45	19	1.1	422	22	AAH46045	Human DNA encoding

ALIGNMENTS

RESULT 1

AAH43683
ID AAH43683 standard; DNA; 1722 BP.

XX
AC AAH43683;

XX
DT 21-JAN-2002 (first entry)

XX
DE PRKAG3 intron 4 - intron 10.

XX
KW Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
metabolic disease; diabetes; obesity; substitution; ds.

XX
OS Homo sapiens.

XX	Key	Location/Qualifiers
FH	intron	1..13
FT		/tag= a
FT		/number= "Intron 4"
FT		/note= "3' portion of intron 4"
FT	exon	14..95
FT		/tag= b
FT		/number= "Exon 5"
FT	intron	96..552
FT		/tag= c
FT		/number= "Intron 5"
FT	exon	553..611
FT		/tag= d
FT		/number= "Exon 6"
FT	intron	612..736
FT		/tag= e
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FT exon 737..782
FT /*tag= f
FT /number= "Exon 7"
FT intron 783..986
FT /*tag= g
FT /number= "Intron 7"
FT exon 987..1041
FT /*tag= h
FT /number= "Exon 8"
FT intron 1042..1242
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FT exon 1243..1369
FT /*tag= j
FT /number= "Exon 9"
FT intron 1370..1522
FT /*tag= k
FT /number= "Intron 9"
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FT /*tag= l
FT /number= "Exon 10"
FT intron 1689..1722
FT /*tag= i
FT /number= "Intron 10"
FT /note= "5' portion of intron 10"
XX WO200177305-A2.
PN 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-SE00765.
XX
XX 07-APR-2000; 2000US-195665P.
XX (AREX-) AREXIS AB.
XX
XX Andersson L, Luthman H, Marklund S;
XX WPI; 2001-657170/75.
XX
XX New variants of human AMP-activated protein kinase gamma3 subunit
XX associated with a metabolic disease e.g. diabetes or obesity and method
XX for determining a risk estimate of diseases in subject by detecting the
XX variant -
XX
XX Example 1; Fig 3; 25pp; English.
XX
XX The sequences given in AAH43681-84 represents genomic fragments
XX encoding the human AMP-activated protein kinase gamma 3 subunit
XX (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant,
XX is useful in determining a risk estimate of a metabolic disease,
XX such as diabetes or obesity, in a subject. The variation may occur
XX in exons 3, 4 or 10. In exon 3 variation may be a substitution of
XX a G for a C at nucleotide 320, resulting in the amino acid
XX substitution P1A; in exon 4 variation may be a substitution of a
XX T for a C at nucleotide 550; and in exon 10 variation may be a
XX substitution of a T for a C at nucleotide 1037, resulting in the
XX amino acid substitution R340W. There may also be nucleotide variation
XX in intron 6.
XX
XX Sequence 1722 BP; 321 A; 504 C; 534 G; 363 T; 0 other;
XX
XX Query Match 100.0%; Score 1722; DB 22; Length 1722;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1722; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX 1 CCTGGCCCCCTCAGATCAAGAACGGCTTCTTGGCTGGGCCCAACGGTGGCGGAGC 60
XX Db 1 CCTGGCCCCCTCAGATCAAGAACGGCTTCTTGGCTGGGCCCAACGGTGGCGGAGC 60
XX
XX 61 CCCTCTATGGGACAGCAAGAACGAGAGCTTTGGGCTGACGAGAGCTGGGAGGTGAAG 120
XX Db 61 CCCTCTATGGGACAGCAAGAACGAGAGCTTTGGGCTGACGAGAGCTGGGAGGTGAAG 120
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OY 1201 CTCCTAGGCTGCCCGAGGCTCACTGCTCCCATCTCTGCAGCCTGTTGAAGCTGTCTA 1260
Db 1201 CTCCTAGGCTGCCCGAGGCTCACTGCTCCCATCTCTGCAGCCTGTTGAAGCTGTCTA 1260
OY 1261 CACCTCATCAAGAACCGGATCCATCGCTGCCCTGTTCTTGACCCGGTGTCAAGCAACGT 1320
Db 1261 CACCTCATCAAGAACCGGATCCATCGCTGCCCTGTTCTTGACCCGGTGTCAAGCAACGT 1320
OY 1321 ACTCCATCTTACACACAAACCGCTGCTCAAGTTCCTGACATCTTTTGAAGCCTGGG 1380
Db 1321 ACTCCATCTTACACACAAACCGCTGCTCAAGTTCCTGACATCTTTTGAAGCCTGGG 1380
OY 1381 CCCAGTGGGAGGAAGGGGAGACCTGGGAGGTGATCAGAGGCGCTGAGGAGTCTTCAG 1440
Db 1381 CCCAGTGGGAGGAAGGGGAGACCTGGGAGGTGATCAGAGGCGCTGAGGAGTCTTCAG 1440
OY 1441 CCTAGCAGTCTGGGGAAGAGCTGGGAGCCCTCTTTGAAGCTCTGGATCCCTGATCTCC 1500
Db 1441 CCTAGCAGTCTGGGGAAGAGCTGGGAGCCCTCTTTGAAGCTCTGGATCCCTGATCTCC 1500
OY 1501 ACCTGGTCCCATCTTAACCAAGGTTCCCTGCTGCCCCGGCCCTCTCTCTACCGCAC 1560
Db 1501 ACCTGGTCCCATCTTAACCAAGGTTCCCTGCTGCCCCGGCCCTCTCTCTACCGCAC 1560
OY 1561 TATCCAAGATTTGGGCATCGGCACATTTCCGAGACTTTGGCTGTGCTGCGAGACAGCAC 1620
Db 1561 TATCCAAGATTTGGGCATCGGCACATTTCCGAGACTTTGGCTGTGCTGCGAGACAGCAC 1620
OY 1621 CATCTGACTGCACTGGACATCTTTTGTGGACCGCGTGTCTGCACTGCCTGTGGTCAA 1680
Db 1621 CATCTGACTGCACTGGACATCTTTTGTGGACCGCGTGTCTGCACTGCCTGTGGTCAA 1680
OY 1681 CGAATGTGGTACCCACCCAGGATGAGAGGCTCGGGCTGGA 1722
Db 1681 CGAATGTGGTACCCACCCAGGATGAGAGGCTCGGGCTGGA 1722
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RESULT 2

ABA44706/c

ID ABA44706 standard; DNA; 378 BP.

XX AC

XX AC

XX AC

XX 01-FEB-2002 (first entry)

XX Human breast cell single exon nucleic acid probe #3401.

XX Human; microarray; single exon probe; gene expression; breast;

XX disease; cancer; ss.

XX Homo sapiens.

XX WO200157271-A2.

XX PD

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00662.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-496933/54.

XX New spatially-addressable set of single exon nucleic acid probes,

XX PT

PT useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -

XX Claim 1; SEQ ID NO 3401; 327bp + sequence listing; English.

XX The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;

Query Match 20.1%; Score 346; DB 22; Length 378;

Best Local Similarity 100.0%; Pred. No. 1.6e-148;

Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCTGCCCCCTCAGATCAAGAAGGCGCTTCTTTGCTCTGCTGCCCAACGGTGTCCGGGCAGC 60

Db 362 CCTGCCCCCTCAGATCAAGAAGGCGCTTCTTTGCTCTGCTGCCCAACGGTGTCCGGGCAGC 303

OY 61 CCTCTATGGGACAGCAAGAGGAGCTTTGCTGCTGCTGCCCAACGGTGTCCGGGCAGC 120

Db 302 CCTCTATGGGACAGCAAGAGGAGCTTTGCTGCTGCTGCCCAACGGTGTCCGGGCAGC 243

OY 121 GGAGATGAGGAGGTGAGGGGAGATCTTGATCGTGTGTTCTGGGGCTGATCTCTGATAT 180

Db 242 GGAGATGAGGAGGTGAGGGGAGATCTTGATCGTGTGTTCTGGGGCTGATCTCTGATAT 183

OY 181 ACCACAGCTTTGGCTTCAGGCCAAGCCAGCCAGGGGCGAGGTTGGAGAAAGTCCATCC 240

Db 182 ACCACAGCTTTGGCTTCAGGCCAAGCCAGCCAGGGGCGAGGTTGGAGAAAGTCCATCC 123

OY 241 GGAGTCTGCATGGCCAGCTGGGAGACCTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 300

Db 122 GGAGTCTGCATGGCCAGCTGGGAGACCTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 63

OY 301 ATGACCAAGTGCACACCTTTTCACTCCGCTACTGCATGCCCTGTGC 346

Db 62 ATGACCAAGTGCACACCTTTTCACTCCGCTACTGCATGCCCTGTGC 17

RESULT 3

ABAS5162/c

ID ABAS5162 standard; DNA; 378 BP.

XX AC

XX AC

XX AC

XX 01-FEB-2002 (first entry)

XX Human foetal liver single exon nucleic acid probe #3467.

XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

XX Homo sapiens.

XX WO200157277-A2.

XX 09-AUG-2001.

XX

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PF 30-JAN-2001; 2001WO-US00669.
XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human fetal liver -
XX
XX Claim 1; SEQ ID NO 3467; 639pp + sequence listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for
XX measuring human gene expression in a sample derived from human foetal
XX liver. The single exon nucleic acid probes may be used for predicting,
XX measuring and displaying gene expression in samples derived from human
XX fetal liver. The present sequence is a single exon nucleic acid
XX probe of the invention.
XX
XX Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;

Query Match      20.1%; Score 346; DB 22; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.6e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGCCCTCAGATCAAGAAGCCCTTCTTGGTGTGAGAGAGCTTGTGGGCTGATCTCTGATAT 60
DB |||||||
DB 362 CCTGGCCCTCAGATCAAGAAGCCCTTCTTGGTGTGAGAGAGCTTGTGGGCTGATCTCTGATAT 303
QY 61 CCTCTATGGGACAGCAAGACGAGCTTTGTGGGTGAGAGAGCTTGTGGGAGGTGAAG 120
DB |||||||
DB 302 CCTCTATGGGACAGCAAGACGAGCTTTGTGGGTGAGAGAGCTTGTGGGAGGTGAAG 243
QY 121 GGAGATGGAGAGGTGAGGGGAGATCTTGACGGTGTCTTCTGGGGCTGATCTCTGATAT 180
DB |||||||
DB 242 GGAGATGGAGAGGTGAGGGGAGATCTTGACGGTGTCTTCTGGGGCTGATCTCTGATAT 183
QY 181 ACCACAAGCTTGGCTTTCAGGCCAAGCCAGCCAGGGGCCAGGGTGGAGAAAGTCCATCC 240
DB |||||||
DB 182 ACCACAAGCTTGGCTTTCAGGCCAAGCCAGCCAGGGGCCAGGGTGGAGAAAGTCCATCC 123
QY 241 GGAGTCTGCATGGCCAGCTGGAGACCTTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 300
DB |||||||
DB 122 GGAGTCTGCATGGCCAGCTGGAGACCTTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 63
QY 301 ATGACAGCTGACACTTTCACCTCCGCTACTGCGATGCCCTGTGC 346
DB |||||||
DB 62 ATGACAGCTGACACTTTCACCTCCGCTACTGCGATGCCCTGTGC 17

RESULT 4
ABA24907/c
ID ABA24907 standard; DNA; 378 BP.
XX
XX ABA24907;
AC
XX
XX 23-JAN-2002 (first entry)
XX
XX Probe #3373 for gene expression analysis in human heart cell sample.
XX Human; gene expression; heart; microarray; vascular system; probe;
KW
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KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX
XX Homo sapiens.
XX
XX WO200157274-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00666.
XX
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488899/53.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX hearts -
XX
XX Claim 1; SEQ ID NO 3373; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart. The
XX present sequence is one such probe. The probes may be used for
XX predicting, measuring and displaying gene expression in samples derived
XX from the human heart via microarrays. By measuring gene expression, the
XX probes are useful for predicting, diagnosing, grading, staging,
XX monitoring and prognosing diseases of the human heart and vascular system
XX e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX congenital heart disease.
XX
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
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Query Match      20.1%; Score 346; DB 22; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.6e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGCCCTCAGATCAAGAAGCCCTTCTTGGTGTGAGAGAGCTTGTGGGCTGATCTCTGATAT 60
DB |||||||
DB 362 CCTGGCCCTCAGATCAAGAAGCCCTTCTTGGTGTGAGAGAGCTTGTGGGCTGATCTCTGATAT 303
QY 61 CCTCTATGGGACAGCAAGACGAGCTTTGTGGGTGAGAGAGCTTGTGGGAGGTGAAG 120
DB |||||||
DB 302 CCTCTATGGGACAGCAAGACGAGCTTTGTGGGTGAGAGAGCTTGTGGGAGGTGAAG 243
QY 121 GGAGATGGAGAGGTGAGGGGAGATCTTGACGGTGTCTTCTGGGGCTGATCTCTGATAT 180
DB |||||||
DB 242 GGAGATGGAGAGGTGAGGGGAGATCTTGACGGTGTCTTCTGGGGCTGATCTCTGATAT 183
QY 181 ACCACAAGCTTGGCTTTCAGGCCAAGCCAGCCAGGGGCCAGGGTGGAGAAAGTCCATCC 240
DB |||||||
DB 182 ACCACAAGCTTGGCTTTCAGGCCAAGCCAGCCAGGGGCCAGGGTGGAGAAAGTCCATCC 123
QY 241 GGAGTCTGCATGGCCAGCTGGAGACCTTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 300
DB |||||||
DB 122 GGAGTCTGCATGGCCAGCTGGAGACCTTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 63
QY 301 ATGACAGCTGACACTTTCACCTCCGCTACTGCGATGCCCTGTGC 346
DB |||||||
DB 62 ATGACAGCTGACACTTTCACCTCCGCTACTGCGATGCCCTGTGC 17
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RESULT 5
AAK03423/C
ID AAK03423 standard; DNA; 378 BP.
XX AC AAK03423;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe SEQ ID NO: 3414.
XX
KW Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00667.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
XX brains -
XX
PS Example 4; SEQ ID NO: 3414; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention.
XX
SQ Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
Query Match 20.1%; Score 346; DB 22; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.6e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCTGGCCCTCAGATCAAGAAGGCTTTCTTGCTGCTGGTGGCCAAACGGTGGCGGCAGC 60
Db 362 CCTGGCCCTCAGATCAAGAAGGCTTTCTTGCTGCTGGTGGCCAAACGGTGGCGGCAGC 303
Qy 61 CCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGTGGAGGAGGCTGGGAGGTGAAG 120
Db 302 CCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGTGGAGGAGGCTGGGAGGTGAAG 243
Qy 121 GGAGATGGAGGAGGTGAGGGGAGATCTTGTACGGTTGTTCTGGGCTGATCTCTGATAT 180
Db 242 GGAGATGGAGGAGGTGAGGGGAGATCTTGTACGGTTGTTCTGGGCTGATCTCTGATAT 183
Qy 181 ACCACAAGCTTGGCTTCAGGCCAAGCCAGCCAGGGCCAGGGTGGAGGAAGTCCATCC 240
Db 182 ACCACAAGCTTGGCTTCAGGCCAAGCCAGCCAGGGCCAGGGTGGAGGAAGTCCATCC 123
Qy 241 GGAGTCTGCATGGCCAGCTGGGAGACCCCTGGGGCTCAATTTCCCACTCTGTGGAGCCGCT 300

Db 122 GGAGTCTGCATGGCCAGCTGGGAGACCCCTGGGGCTCAATTTCCCACTCTGTGGAGCCGCT 63
Qy 301 ATGACCAGCTGACACCTTTTACCTCCGCTACTGTCATGCCCCCTGTGC 346
Db 62 ATGACCAGCTGACACCTTTTACCTCCGCTACTGTCATGCCCCCTGTGC 17

RESULT 6
AAK28874/C
ID AAK28874 standard; DNA; 378 BP.
XX AC AAK28874;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed single exon probe SEQ ID NO: 3431.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
OS Homo sapiens.
XX
PN WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00668.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488900/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human bone marrow -
XX
PS Example 4; SEQ ID NO: 3431; 658pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention.
XX
SQ Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
Query Match 20.1%; Score 346; DB 22; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.6e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCTGGCCCTCAGATCAAGAAGGCTTTCTTGCTGCTGGTGGCCAAACGGTGGCGGCAGC 60
Db 362 CCTGGCCCTCAGATCAAGAAGGCTTTCTTGCTGCTGGTGGCCAAACGGTGGCGGCAGC 303
Qy 61 CCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGTGGAGGAGGCTGGGAGGTGAAG 120
Db 302 CCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGTGGAGGAGGCTGGGAGGTGAAG 243
Qy 121 GGAGATGGAGGAGGTGAGGGGAGATCTTGTACGGTTGTTCTGGGCTGATCTCTGATAT 180
Db 242 GGAGATGGAGGAGGTGAGGGGAGATCTTGTACGGTTGTTCTGGGCTGATCTCTGATAT 183
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QY 181 ACCACAGCTTGGCTTCAGGCCAAGCCAGCCAGGGCCAGGGTGGAGGAAGTCCATCC 240
Db 182 ACCACAGCTTGGCTTCAGGCCAAGCCAGCCAGGGCCAGGGTGGAGGAAGTCCATCC 123
QY 241 GGAGTCTGCATGGCCAGCTGGGAGACCCCTGGGGCTCAATTTCCCATCTCTGGAGCCGCT 300
Db 122 GGAGTCTGCATGGCCAGCTGGGAGACCCCTGGGGCTCAATTTCCCATCTCTGGAGCCGCT 63
QY 301 ATGACCACTGACACCTTTCACCTCCGCTACTGATGCGCCCTGTGC 346
Db 62 ATGACCACTGACACCTTTCACCTCCGCTACTGATGCGCCCTGTGC 17

RESULT 7
AAI13465/c
ID AAI13465 standard; DNA; 378 BP.
XX
AC AAI13465;
XX
DT 12-OCT-2001 (first entry)
XX
DE Probe #3398 for gene expression analysis in human cervical cell sample.
XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer; ss.
XX
OS Homo sapiens.
XX
PN W0200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00670.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488901/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -
XX
PS Claim 25; SEQ ID No 3398; 487pp; English.
XX
CC The present invention relates to human single exon nucleic acid probes
CC (SENP). The present sequence is one such probe. The SENPs are derived
CC from human HeLa cells. The SENPs can be used to produce a single exon
CC microarray, which can be used for measuring human gene expression in a
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging
CC of diseases of the cervix, notably cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;

Query Match 20.1%; Score 346; DB 22; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.6e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGCCCTCAGATCAAGAGCCCTTCTTCTGTTGGCCACGCTGTGGCGGAGC 60
Db 362 CCTGGCCCTCAGATCAAGAGCCCTTCTTCTGTTGGCCACGCTGTGGCGGAGC 303

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QY 61 CCCTCTATGGGACAGCAAGAGCAGAGCTTTGTGGGTGAGGAGAGCTGGGAGGTGAAG 120
Db 302 CCCTCTATGGGACAGCAAGAGCAGAGCTTTGTGGGTGAGGAGAGCTGGGAGGTGAAG 243
QY 121 GGAGATGAGGAGGTGAGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGATAT 180
Db 242 GGAGATGAGGAGGTGAGGGGAGATCTTGTACGGTTGTTCTGGGGCTGATCTCTGATAT 183
QY 181 ACCAAGCTTTGGCTTCAGGCCAAGCCAGCCAGGGCCAGGGTGGAGGAAGTCCATCC 240
Db 182 ACCAAGCTTTGGCTTCAGGCCAAGCCAGCCAGGGCCAGGGTGGAGGAAGTCCATCC 123
QY 241 GGAGTCTGCATGGCCAGCTGGGAGACCCCTGGGGCTCAATTTCCCATCTCTGGAGCCGCT 300
Db 122 GGAGTCTGCATGGCCAGCTGGGAGACCCCTGGGGCTCAATTTCCCATCTCTGGAGCCGCT 63
QY 301 ATGACCACTGACACCTTTCACCTCCGCTACTGATGCGCCCTGTGC 346
Db 62 ATGACCACTGACACCTTTCACCTCCGCTACTGATGCGCCCTGTGC 17

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RESULT 8
AAI134821/c
ID AAI134821 standard; DNA; 378 BP.
XX
AC AAI134821;
XX
DT 17-OCT-2001 (first entry)
XX
DE Probe #3507 used to measure gene expression in human placenta sample.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN W0200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00663.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488997/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
XX
PS Claim 25; SEQ ID No 3507; 654pp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENP).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders.
XX
SQ Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;

Query Match 20.1%; Score 346; DB 22; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.6e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CCTGGCCCTCAGATCAAGAGCCCTTTCTTCTCTGCTGGCCCAACGGTGTGCGGGCAGC 60
    |||
Db 362 CTGCGCCCTCAGATCAAGAGCCCTTTCTTCTCTGCTGGCCCAACGGTGTGCGGGCAGC 303
    |||
Qy 61 CCTCTATGGGACACAAAGACAGAGCTTTGTGGGTGAGGAGGCTGGGAGGTGAAG 120
    |||
Db 302 CCTCTATGGGACACAAAGACAGAGCTTTGTGGGTGAGGAGGCTGGGAGGTGAAG 243
    |||
Qy 121 GGAGATGAGGAGGTGAGGGGAGATCTTTGTACGGTGTCTTCTGGGCTGTATCTTGATAT 180
    |||
Db 242 GGAGATGAGGAGGTGAGGGGAGATCTTTGTACGGTGTCTTCTGGGCTGTATCTTGATAT 183
    |||
Qy 181 ACCACAAGCTTGGCTTCAGGCCAAGCCAGCCAGGGCCAGGGTGGAGAAAGTCCATCC 240
    |||
Db 182 ACCACAAGCTTGGCTTCAGGCCAAGCCAGCCAGGGCCAGGGTGGAGAAAGTCCATCC 123
    |||
Qy 241 GGAGTCTCATGGCCAGCTGGGAGACCTTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 300
    |||
Db 122 GGAGTCTCATGGCCAGCTGGGAGACCTTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 63
    |||
Qy 301 ATGACCACTGACACCTTTCACCTCCGCTACTGATGATGCCCTGTGC 346
    |||
Db 62 ATGACCACTGACACCTTTCACCTCCGCTACTGATGATGCCCTGTGC 17
    |||

RESULT 9
AAI03344/c
ID AAI03344 standard; DNA; 378 BP.
XX AC AAI03344;
XX XX
XX DT 09-OCT-2001 (first entry)
XX DE
XX PE Probe #3335 used to measure gene expression in human breast sample.
XX KW Probe; human; breast disease; breast cancer; development disorder; es;
XX KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX OS Homo sapiens.
XX XX
XX PN WO200157270-A2.
XX PD
XX PF 09-AUG-2001.
XX XX
XX PR 29-JAN-2001; 2001WO-US00661.
XX PR
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX XX
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PI WPI; 2001-476286/51.
XX DR
XX PT Novel single exon nucleic acid probe used to measuring gene expression
XX PT in a human breast -
XX PF
XX PS Claim 25; SEQ ID No 3335; 322pp; English.
XX CC
XX CC The present invention relates to novel single exon nucleic acid probes.
XX CC The present sequence is one such probe. The probes are useful for
XX CC measuring human gene expression in a human breast sample, where the probe
XX CC hybridises at high stringency to a nucleic acid expressed in the human
XX CC breast. The probes are useful for predicting, diagnosing, grading,
XX CC staging, monitoring and prognosing diseases of the human breast,
XX CC particularly those diseases with polygenic aetiology. The diseases
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CC include: breast cancer, disorders of development, inflammatory diseases
CC of the breast, fibrocystic changes, proliferative breast disease and
CC non-carcinoma tumours.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
```

```
Query Match 20.1%; Score 346; DB 22; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.6e-148; Indels 0; Gaps 0;
Matches 346; Conservative 0; Mismatches 0;

Qy 1 CTGCGCCCTCAGATCAAGAGCCCTTTCTTCTCTGCTGGCCCAACGGTGTGCGGGCAGC 60
    |||
Db 362 CTGCGCCCTCAGATCAAGAGCCCTTTCTTCTCTGCTGGCCCAACGGTGTGCGGGCAGC 303
    |||
Qy 61 CCTCTATGGGACACAAAGACAGAGCTTTGTGGGTGAGGAGGCTGGGAGGTGAAG 120
    |||
Db 302 CCTCTATGGGACACAAAGACAGAGCTTTGTGGGTGAGGAGGCTGGGAGGTGAAG 243
    |||
Qy 121 GGAGATGAGGAGGTGAGGGGAGATCTTTGTACGGTGTCTTCTGGGCTGTATCTTGATAT 180
    |||
Db 242 GGAGATGAGGAGGTGAGGGGAGATCTTTGTACGGTGTCTTCTGGGCTGTATCTTGATAT 183
    |||
Qy 181 ACCACAAGCTTGGCTTCAGGCCAAGCCAGCCAGGGCCAGGGTGGAGAAAGTCCATCC 240
    |||
Db 182 ACCACAAGCTTGGCTTCAGGCCAAGCCAGCCAGGGCCAGGGTGGAGAAAGTCCATCC 123
    |||
Qy 241 GGAGTCTCATGGCCAGCTGGGAGACCTTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 300
    |||
Db 122 GGAGTCTCATGGCCAGCTGGGAGACCTTGGGGCTCAATTTCCCATCTGTGGAGCCGCT 63
    |||
Qy 301 ATGACCACTGACACCTTTCACCTCCGCTACTGATGATGCCCTGTGC 346
    |||
Db 62 ATGACCACTGACACCTTTCACCTCCGCTACTGATGATGCCCTGTGC 17
    |||
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RESULT 10
ABS03407/c
ID ABS03407 standard; DNA; 378 BP.
XX AC ABS03407;
XX XX
XX DT 19-AUG-2002 (first entry)
XX DE
XX DE Human genome-derived single exon probe from lung SEQ ID No 3398.
XX KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
XX KW chronic obstructive pulmonary disease; interstitial lung disease;
XX KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
XX KW tuberosus sclerosis; Gaucher's disease; Niemann-Pick disease;
XX KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
XX KW pulmonary histiocytosis; lymphangiomyomatosis; Karagener syndrome;
XX KW primary alveolar proteinosis; fibrocystic pulmonary dysplasia;
XX KW primary ciliary dyskinesia; pulmonary hypertension;
XX KW hyaline membrane disease.
XX OS Homo sapiens.
XX XX
XX PN WO200186003-A2.
XX XX
XX PD 15-NOV-2001.
XX PF
XX PF 30-JAN-2001; 2001WO-US00665.
XX XX
XX PR 04-FEB-2000; 2000US-180312P.
XX PR 26-MAY-2000; 2000US-207456P.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-234687P.
XX PR 27-SEP-2000; 2000US-236359P.
XX PR 04-OCT-2000; 2000GB-0024263.
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XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX XX WPI; 2002-114183/15.
XX PT Spatially-addressable set of single exon nucleic acid probes, used to
XX PT measure gene expression in human lung samples -
XX PS Claim 1; SEQ ID No 3398; 634pp; English.
XX CC The invention relates to a spatially-addressable set of single exon
XX CC nucleic acid probes for measuring gene expression in a sample derived
XX CC from human lung comprising single exon nucleic acid probes having one of
XX CC 12614 nucleic acid sequences mentioned in the specification, or their
XX CC complements or the 12397 open reading frames derived from the 12614
XX CC probes. Also included are a microarray comprising the novel set of
XX CC probes; the novel set of probes which hybridise at high stringency to a
XX CC nucleic acid expressed in the human lung; measuring gene expression in a
XX CC sample derived from human lung, comprising (a) contacting the array with
XX CC a collection of detectably labeled nucleic acids derived from human lung
XX CC mRNA, and (b) measuring the label detectably bound to each probe of
XX CC the array; identifying exons in a eukaryotic genome, comprising
XX CC (a) algorithmically predicting at least one exon from genomic sequences
XX CC of the eukaryote; and (b) detecting specific hybridisation of detectably
XX CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
XX CC having a fragment identical to the predicted exon, the probe is included
XX CC in the above mentioned microarray; assigning exons to a single gene,
XX CC comprising (a) identifying exons from genomic sequence by the method
XX CC above and (b) measuring the expression of each of the exons in several
XX CC tissues and/or cell types using hybridisation to a single exon
XX CC microarrays having a probe with the exon, where a common pattern of
XX CC expression of the exons in the tissues and/or cell types indicates that
XX CC the exons should be assigned to a single gene; a peptide comprising one
XX CC of 12011 sequences, mentioned in the specification, or encoded by the
XX CC probes/open reading frames (ORF). The probes are used for gene
XX CC expression analysis, and for identifying exons in a gene, particularly
XX CC using human lung derived mRNA and for the study of lung diseases
XX CC such as asthma, lung cancer, chronic obstructive pulmonary disease
XX CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
XX CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
XX CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
XX CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
XX CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic
XX CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension
XX CC and hyaline membrane disease. The present sequence is a single exon
XX CC probe of the invention.
XX CC Note: The sequence data for this patent did not form part
XX CC of the printed specification, but was obtained in electronic
XX CC format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
Query Match 20.1%; Score 346; DB 24; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.6e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTGGCCCTCAGATCAAGAAGCCCTTCTTGCTGTGGCCCAACGGTGTGCGGCGAGC 60
DB 362 CCTGGCCCTCAGATCAAGAAGCCCTTCTTGCTGTGGCCCAACGGTGTGCGGCGAGC 303
QY 61 CCTCTATGGACAGCAAGACAGAGCTTTGTGGGTGAGGAGAGCGCTGGGAGGTGAAG 120
DB 302 CCTCTATGGACAGCAAGACAGAGCTTTGTGGGTGAGGAGAGCGCTGGGAGGTGAAG 243
QY 121 GGAGATGGAGAGGTCAGGGGAGATCTTGACGGTTGTTCTGGGGCTGATCTTGATAT 180
DB 242 GGAGATGGAGAGGTCAGGGGAGATCTTGACGGTTGTTCTGGGGCTGATCTTGATAT 183
QY 181 ACCACAAGCTTGGCTTTACGCCCAAGCCAGCCAGGGGGCCAGGGTGGAGGAAGTCCATCC 240
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DB 182 ACCAACAAGTTGGCTTTCAGGCCAAGCCAGCCAGGGGCCAGGGTGGAGAAAGTCCATCC 123
QY 241 GGAGTCTGCATGGCCAGCTGGGAGACCTGGGGCTCAATTTCCCATCTCTGGAGCGCT 300
|||||
DB 122 GGAGTCTGCATGGCCAGCTGGGAGACCTGGGGCTCAATTTCCCATCTCTGGAGCGCT 63
QY 301 ATGACCAGCTGACACCTTTTACCTCCGCTACTGCATGCGCCCTGTGC 346
|||||
DB 62 ATGACCAGCTGACACCTTTTACCTCCGCTACTGCATGCGCCCTGTGC 17

RESULT 11
AAH43685
ID AAH43685 standard; cDNA; 1647 BP.
XX AC AAH43685;
XX DT 21-JAN-2002 (first entry)
XX DE PRKAG3 cDNA.
XX KW Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
XX KW metabolic disease; diabetes; obesity; substitution; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX CDS 20..1489
FT variation /*tag= a
FT /*product= "PRKAG3"
FT /*tag= b
FT /label= "C230G"
FT variation /*tag= c
FT /*tag= c
FT /label= "T559C"
FT variation /*tag= d
FT /label= "C1037T"
FT /*note= "Causes P71A"
FT /*tag= c
FT /label= "T559C"
FT variation /*tag= d
FT /label= "C1037T"
FT /*note= "Causes R340W"
XX WO200177305-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-SE00765.
XX PR 07-APR-2000; 2000US-195665P.
XX PA (AREX-) AREXIS AB.
XX PI Andersson L, Luthman H, Marklund S;
XX WPI; 2001-657170/75.
XX P-PSDB; Q0847679.
XX PT New variants of human AMP-activated protein kinase gamma3 subunit
XX PT associated with a metabolic disease e.g. diabetes or obesity and method
XX PT for determining a risk estimate of diseases in subject by detecting the
XX PT variant -
XX PS Disclosure; Fig 5; 25pp; English.
XX CC This sequence represents the full length cDNA encoding the human
XX CC AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting
XX CC the presence of the PRKAG3 DNA, or a variant, is useful in determining
XX CC a risk estimate of a metabolic disease, such as diabetes or obesity,
XX CC in a subject. The variation may occur in exons 3, 4 or 10. In exon
XX CC 3 variation may be a substitution of a G for a C at nucleotide 320,
XX CC resulting in the amino acid substitution P71A; in exon 4 variation may
XX CC be a substitution of a T for a C at nucleotide 550; and in exon 10
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CC variation may be a substitution of a T for a C at nucleotide 1037,
 CC resulting in the amino acid substitution R340W. There may also be
 CC nucleotide variation in intron 6. The numbering of these
 CC variations is based on the full length cDNA as given, rather than on
 CC position 1 of the open reading frame.

XX
 SQ Sequence 1647 BP; 346 A; 502 C; 462 G; 337 T; 0 other;
 Query Match 9.8%; Score 168; DB 22; Length 1647;
 Best Local Similarity 100.0%; Pred. No. 6e-67;
 Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1523 GGTTCCTGCTGCCCCGCCCTCTCTACCGCACTATCCAAAGATTGGGCATCGGC 1582
 Db 1022 GGTTCCTGCTGCCCCGCCCTCTCTCTACCGCACTATCCAAAGATTGGGCATCGGC 1081
 Qy 1583 ACATTCCGAGACTTGGCTGGTCTGGAGACAGACACCCATCTGACTGCGACATC 1642
 Db 1082 ACATTCCGAGACTTGGCTGGTCTGGAGACAGACACCCATCTGACTGCGACATC 1141
 Qy 1643 TTTGTGGACCGCGCTGTCTGCACTCCCTGTGTCACCAAGATGTGGT 1690
 Db 1142 TTTGTGGACCGCGCTGTCTGCACTCCCTGTGTCACCAAGATGTGGT 1189

RESULT 12
 AAD03296
 ID AAD03296 standard; DNA; 2109 BP.

XX AC AAD03296;
 XX DT 13-JUN-2001 (first entry)
 XX DE Human AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.
 KW Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
 KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
 KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
 KW cystathione beta synthase; CBS; cardiant; gene therapy; ss.
 XX OS Homo sapiens.

XX Key Location/Qualifiers
 FH 5'UTR 1..471
 FT /*tag= a
 FT CDS 472..1389
 FT /*tag= b
 FT FT /product= "Human Prkag3 protein"
 FT 3'UTR 1390..2109
 FT /*tag= c

XX WO200120003-A2.
 XX 22-MAR-2001.
 XX 11-SEP-2000; 2000WO-EP09896.
 XX 10-SEP-1999; 99EP-0402236.
 PR 18-MAY-2000; 2000EP-0401388.
 XX (INRG) INRA INST NAT RECH AGRONOMIQUE.
 PA (ANDE/) ANDERSSON L.
 PA (LOOF/) LOOFT C.
 PA (KALM/) KALM E.
 XX Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
 PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;
 XX WPI: 2001-244810/25.
 DR P-PSDB; AAE00221.

XX New variants of the gamma subunit of vertebrate adenosine
 PT monophosphate-activated kinase for diagnosis or treatment of disorders

PT associated with energy metabolism such as diabetes, obesity, and
 PT myopathy -
 XX Claim 12; Fig 2; 71pp; English.

XX The present sequence is a cDNA encoding human adenosine monophosphate
 CC (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,
 CC PRKAG3. Mutation in Prkag3 results in an altered regulation of
 CC carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is
 CC useful as therapeutic for treating carbohydrate metabolism disorders such
 CC as diabetes, obesity, and disorders associated with muscle metabolism
 CC such as myopathy and cardiovascular diseases, to modulate AMPK
 CC activity, and for restoring a normal AMPK function. PRKAG3 sequence
 CC and its functionally altered mutants are useful for the diagnostic
 CC evaluation, genetic testing and prognosis of a metabolic disorder,
 CC preferably a carbohydrate metabolism disorder. Primers that can detect
 CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
 CC useful for detecting a dysfunction of carbohydrate metabolism resulting
 CC from the expression of a functionally altered allele of PRKAG3.
 CC Transgenic animal and host cell transformed with PRKAG3 or a
 CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
 CC screening compounds able to modulate AMPK activity. Nucleic acid
 CC encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
 CC in a sequence encoding the first cystathione beta synthase (CBS) domain
 CC of PRKAG3 and is useful in gene therapy.

XX SQ Sequence 2109 BP; 458 A; 621 C; 560 G; 470 T; 0 other;

Query Match 9.8%; Score 168; DB 22; Length 2109;
 Best Local Similarity 100.0%; Pred. No. 5.9e-67;
 Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1523 GGTTCCTGCTGCCCCGCCCTCTCTACCGCACTATCCAAAGATTGGGCATCGGC 1582
 Db 922 GGTTCCTGCTGCCCCGCCCTCTCTCTACCGCACTATCCAAAGATTGGGCATCGGC 981
 Qy 1583 ACATTCCGAGACTTGGCTGGTCTGGAGACAGACACCCATCTGACTGCGACATC 1642
 Db 982 ACATTCCGAGACTTGGCTGGTCTGGAGACAGACACCCATCTGACTGCGACATC 1041
 Qy 1643 TTTGTGGACCGCGCTGTCTGCACTCCCTGTGTCACCAAGATGTGGT 1690
 Db 1042 TTTGTGGACCGCGCTGTCTGCACTCCCTGTGTCACCAAGATGTGGT 1089

RESULT 13
 AAD03320
 ID AAD03320 standard; cDNA; 2115 BP.

XX AC AAD03320;
 XX DT 13-JUN-2001 (first entry)
 XX DE Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.
 DE KW Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
 KW PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
 KW genetic testing; carbohydrate metabolism disorder; skeletal muscle;
 KW cystathione beta synthase; CBS; cardiant; gene therapy; ss.
 XX OS Homo sapiens.

XX Key Location/Qualifiers
 FH CDS 1..1395
 FT /*tag= a
 FT /product= "Human complete Prkag3 protein"
 XX WO200120003-A2.
 XX 22-MAR-2001.
 XX 11-SEP-2000; 2000WO-EP09896.


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XX SQ Sequence 547 BP; 112 A; 172 C; 133 G; 130 T; 0 other;
Query Match      8.5%; Score 147; DB 22; Length 547;
Best Local Similarity 100.0%; Pred. No. 2.8e-57;
Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1523 GGTTCCTCTGCTGCCCGCCCTCTCTCTACCGCACTATCCAGATTTGGGATCGGC 1582
Db      |||||||
QY 1583 ACATTCCGAGACTTGGCTGTGGTGTGGAGACAGCACCACCTCTGACTGCACTGGACATC 1642
Db      |||||||
QY 1643 TTTGTGGACCGCGGTGTCTGCACTG 1669
Db      |||||||
QY 405 TTTGTGGACCGCGGTGTCTGCACTG 431

RESULT 15
ABA49850/c
ID ABA49850 standard; DNA; 92 BP.
XX AC ABA49850;
XX DT 01-FEB-2002 (first entry)
XX DE Human breast cell single exon nucleic acid probe #8545.
XX KW Human; microarray; single exon probe; gene expression; breast;
XX KW disease; cancer; ss.
XX OS Homo sapiens.
XX PN WO200157271-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000662.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-496933/54.
XX New spatially-addressable set of single exon nucleic acid probes,
PT useful for measuring gene expression in sample derived from human
PT breast, comprises number of single exon nucleic acid probes -
XX
PS Claim 4; SEQ ID NO 8545; 327pp + sequence listing; English.
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting
CC the probes with a collection of detectably labelled nucleic acids
CC derived from mRNA of human breast, and then measuring the label
CC bound to each probe of the microarray. The probes are useful for
CC verifying the expression of regions of genomic DNA predicted to
CC encode proteins. They are useful for gene discovery, and for
CC determining predisposition and/or prognosing breast disease. Gene
CC expression analysis is useful for assessing the toxicity of chemical
CC agents on cells. The microarray of this invention presents a far greater
CC diversity of probes for measuring gene expression, with far less bias
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CC than expressed sequence tag microarrays. The method is suitable for
CC rapid production of functional information from genomic sequence. The
CC present sequence is a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 92 BP; 22 A; 24 C; 34 G; 12 T; 0 other;

Query Match 3.8%; Score 65; DB 22; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTGGCCCCCTCAGATCAAGAAGCCCTTCTTTGCTCTGGTGGCCACGGTGTGCGGGCAGC 60
Db 65 CCTGGCCCCCTCAGATCAAGAAGCCCTTCTTTGCTCTGGTGGCCACGGTGTGCGGGCAGC 6

QY 61 CCCTC 65

Db 5 CCCTC 1

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